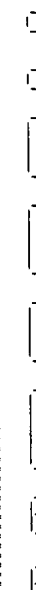


(RL)



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protein - protein database search. using Smith-Waterman algorithm

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Run on: Tue Aug 29 17:04:16 1995; MasPar time 4.86 Seconds
520.987 Million cell updates/sec
Tabular output not generated.
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Title: >US-08-249-671-5
Description: (1:165) from US08249671.pep
Perfect Score: 1222
Sequence: 1 CDLPQTHSLGSRRTIMLLAQ.....

```

Scoring table: PAM 150
Gap 11

Searched: 43470 segs. 15335248 residues

Database: swiss-prot31

statistics: Mean 44.731: Variance 85.676: scale 0.522

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query	Match	Length	DB	ID	Description	Pred. No.
1	1210	99.0	188	4	INA2	HUMAN	INTERFERON ALPHA-2	PR	2.34e-229
2	1074	87.9	189	4	INA5	HUMAN	INTERFERON ALPHA-5	PR	1.12e-199
3	1050	85.9	189	4	INA6	HUMAN	INTERFERON ALPHA-14	P	1.88e-194
4	1049	85.8	189	4	INA6	HUMAN	INTERFERON ALPHA-6	PR	3.09e-194
5	1030	84.3	189	4	INA4	HUMAN	INTERFERON ALPHA-4	PR	4.19e-190
6	1027	84.0	189	4	INA6	HUMAN	INTERFERON ALPHA-21	P	1.88e-189
7	1026	84.0	189	4	INA6	HUMAN	INTERFERON ALPHA-17	P	3.10e-189
8	1025	83.9	189	4	INA6	HUMAN	INTERFERON ALPHA-16	P	5.11e-189
9	1017	83.2	189	4	INA6	HUMAN	INTERFERON ALPHA-10	P	2.79e-187
10	1012	82.8	189	4	INA8	HUMAN	INTERFERON ALPHA-8	PR	3.40e-186

11	1012	82.8	189	4	INA7	HUMAN	INTERFERON ALPHA-7	PR	3.40e-186
12	1010	82.7	189	4	INA1	HUMAN	INTERFERON ALPHA-1/13	9.25e-187	
13	953	78.0	184	4	INA4	HORSE	INTERFERON ALPHA-4	PR	2.13e-173
14	952	77.9	184	4	INA2	HORSE	INTERFERON ALPHA-2	PR	3.50e-173
15	950	77.7	184	4	INA1	HORSE	INTERFERON ALPHA-1	PR	9.49e-173
16	950	77.7	184	4	INA3	HORSE	INTERFERON ALPHA-3	PR	9.49e-173
17	812	66.4	189	4	INA4	BOVIN	INTERFERON ALPHA-A	PR	5.94e-143
18	808	66.1	189	4	INA6	BOVIN	INTERFERON ALPHA-B	PR	4.04e-142
19	805	65.9	189	4	INA5	MOUSE	INTERFERON ALPHA-5	PR	1.78e-141
20	804	65.8	189	4	INA1	BOVIN	INTERFERON ALPHA-1	PR	2.92e-141
21	804	65.8	189	4	INA1	BOVIN	INTERFERON ALPHA-C	PR	2.92e-141
22	798	65.3	189	4	INA1	MOUSE	INTERFERON ALPHA-1	PR	5.67e-140
23	792	64.8	189	4	INA2	BOVIN	INTERFERON ALPHA-D	PR	1.10e-138
24	782	64.0	190	4	INA2	MOUSE	INTERFERON ALPHA-2	PR	1.53e-136
25	775	63.4	192	4	INA1	RAT	INTERFERON ALPHA-1	PR	4.84e-135
26	770	63.0	190	4	INA7	MOUSE	INTERFERON ALPHA-7	PR	2.50e-134
27	767	62.8	190	4	INA1	HUMAN	INTERFERON OMEGA-1	PR	2.70e-133
28	763	62.4	193	4	INA9	MOUSE	INTERFERON ALPHA-9	PR	1.80e-132
29	760	62.2	189	4	INA8	MOUSE	INTERFERON ALPHA-8	PR	7.89e-132
30	760	62.2	189	4	INA6	MOUSE	INTERFERON ALPHA-6	PR	7.89e-132
31	721	59.0	195	4	INA2	HORSE	INTERFERON OMEGA-2	PR	1.70e-123
32	689	56.4	194	4	INA4	FELCA	INTERFERON PRECURSOR	1.11e-116	
33	686	56.1	186	4	INA4	MOUSE	INTERFERON ALPHA-4	PR	4.83e-116
34	677	55.4	195	4	INA1	BOVIN	INTERFERON OMEGA-1	PR	3.95e-114
35	675	55.2	195	4	IND1	HUMAN	INTERFERON DELTA-1	PR	1.05e-113
36	673	55.1	195	7	TP11	BOVIN	TROPHOBLAST PROTEIN-1	2.80e-113	
37	668	54.7	195	7	TP12	BOVIN	TROPHOBLAST PROTEIN-1	3.22e-112	
38	652	54.3	195	7	TP13	BOVIN	TROPHOBLAST PROTEIN-1	3.71e-111	
39	652	53.4	195	4	INA1	HORSE	INTERFERON OMEGA-1	PR	7.97e-109
40	621	50.8	195	7	TP1	SHEEP	TROPHOBLAST PROTEIN-1	2.88e-102	
41	448	36.9	186	4	INB2	BOVIN	INTERFERON BETA-2	PRE	3.37e-66
42	402	32.7	186	4	INB3	BOVIN	INTERFERON BETA-3	PRE	8.15e-57
43	401	32.8	187	4	INB	HUMAN	INTERFERON BETA	PRECU	1.30e-56
44	377	30.9	186	4	INB	HORSE	INTERFERON BETA	PRECU	9.12e-52
45	332	27.2	186	4	INB1	BOVIN	INTERFERON BETA-1	PE	8.64e-43

ALIGNMENTS

RESULT	1
ID	INA2 HUMAN STANDARD; PRG; 188 AA.
AC	P01563; P01564;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE	INTERFERON ALPHA-2 PRECURSOR (INTERFERON ALPHA-A) (LEIF A).
GN	IFNA2.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RM	81052322
RA	GODEL D.V., YELVERTON E., ULLRICH A., HEYNEKER H.L., MIOZZAR
RA	HEIMES W., SEEBURG P.H., DULL T.J., MAY L., STEBBING N., CREA
RA	MADA S., MCCANDLISS R., SILOVA A., TABOR J.M., GROSS M.,
RA	FAMILIETTI P.C., PEŠTKA S.;
RL	NATURE 287:411-416(1980).
RN	[2]
RP	SEQUENCE FROM N.A.
RM	81148795
RA	GODEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAWN R.M.,
RA	MCCANDLISS R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.
RL	NATURE 290:20-26(1981).

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RN [3]
RP SEQUENCE FROM N.A.
RM 82060261
RA LAWN R.M., GROSS M., HOUCK C.M., FRANKS A.E., GRAY P.V.,
RA GOEDDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:5435-5439(1981).
RN [4]
RP SEQUENCE OF 7-188 FROM N.A.
RM 81015442
RA STREULI M., NAGATA S., WEISSMANN C.;
RL SCIENCE 209:1343-1347(1980).
RN [5]
RP SEQUENCE OF 24-112 AND 136-188.
RM 81052321
RA ALLEN G., FANTES K.H.;
RL NATURE 287:408-411(1980).
RN [6]
RP DISULFIDE BONDS.
RM 81123083
RA WEIZEL R.;
RL NATURE 289:606-607(1981).
RN [7]
RP 3D-STRUCTURE MODELLING.
RM 94052087
RA MURGOLO N.J., WINDSOR W.T., HRUZA A., REICHERT P., TSARBOPOULOS A.,
RA BALDWIN S., HUANG E., PRAMANIK B., EALICK S., TROTTE P.P.;
RL PROTEINS 17:62-74(1993).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; V00548; HSIFR6.
DR EMBL; V00549; HSIFR7.
DR PIR; A01827; IVHUA2.
DR PIR; A01828; IVHUA3.
DR PDB; 2HIE; 31-AUG-94.
DR MM; 147562; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON ALPHABETA.
KW CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 23
FT CHAIN 24 188 INTERFERON ALPHA-2.
FT DISULFID 24 121
FT DISULFID 52 161
FT CONFLICT 46 46 K -> R (IN REF. 3 AND 4).
SQ SEQUENCE 188 AA; 21550 MW; 189049 CN;

DB 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 2.34e-229;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdipqthslsrrtllmlaqrkislfcslkrdhdfgfpqeeqngfqaetipvlhemi 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFSCLKDRDRFGFPQEEFGNQFOKAETIPVLHMI 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 84 qqifnlfstkdsaaawdetllldkfyteylqqindleacviggvgvgtetplmkedsilavr 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 61 QQIFNLFSTKDSAAAWDETLLDKFYTELYQQINDLEACVIGGVGTETPLMKEDSILAVR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 144 kyfqrtilylekkykspcawevvraeimsrfslnqlqeslrake 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 121 KYFQRITLYLEKKYKSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 2
ID INA5_HUMAN STANDARD; PRT; 189 AA.

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AC P01569;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON
DE ALPHA-61).
GN IFNA5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 86037205
RA HENCO K., BROSTUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,
RA HOCHSTADT J., KOVACIC T., PASEK M., SCHAMBOECK A., SCHMID J.,
RA TODOKORO K., WAELCHLI M., NAGATA S., WEISSMANN C.;
RL J. MOL. BIOL. 185:227-260(1985).
RN [2]
RP SEQUENCE OF 57-189 FROM N.A.
RM 81148795
RA GOEDDEL D.V., LEDUNG D.W., DULL T.J., GROSS M., LAWN R.M.,
RA MCCANDLISS R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;
RL NATURE 290:20-26(1981).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; X02956; HSIFNA5.
DR EMBL; V00541; HSIFR13.
DR PIR; A01833; IVHUA7.
DR HSP; P01563; 2HIE.
DR MM; 147565; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON ALPHABETA.
KW CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-5.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 189 AA; 21942 MW; 184346 CN;

DB 4; Score 1074; Match 84.9%; QryMatch 87.9%; Pred. No. 1.12e-199;
Matches 141; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

Db 24 cdipqthslsrrtllmlaqrkislfcslkrdhdfgfpqeeqngfqaetipvlhemi 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFSCLKDRDRFGFPQEEFGNQFOKAETIPVLHMI 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 84 iqgfnlfskdsatwdeitldkfyteylqqindleacmqqevgvedtplmrvdsilv 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAAWDETLLDKFYTELYQQINDLEACVIGGVGTETPLMKEDSILAV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

Db 144 kyfqrtilylekkykspcawevvraeimsrfslnqlqeslrake 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 KYFQRITLYLEKKYKSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

RESULT 3
ID INAD_HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LEIF H)
DE (INTERFERON LAMBDA-2-H).

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ID	INA6 HUMAN	STANDARD;	PRT;	189 AA.
AC	P05013;			
DT	13-AUG-1987 (REL. 05, CREATED)			
DDT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)			
DE	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	INTERFERON ALPHA-6 PRECURSOR (INTERFERON ALPHA-K) (LEIF K) (INTERFERON ALPHA-54).			
DGN	INFA6.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
CC	[1]			
CC	SEQUENCE FROM N.A.			
RRM	86037205			
ARA	HENCO K., BROSIUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,			
ARA	HOCHSTADT J., KOVATIC T., PASEK M., SCHAMBECK A., SCHMID J.,			
ARA	TODOKORO K., WAEICHLI M., NAGATA S., WEISSMANN C.;			
JRL	J. MOL. BIOL. 185:227-260(1985).			
CCC	-f- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL			
CCC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:			
CCC	A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.			
CCC	-f- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.			
CCC	EMBL; X02958; HSINFNA6.			
DR	PIR; A23753; IVHU16.			
DR	HSSP; P01563; ZHIIE.			
DR	MIM; 1475663; 11TH EDITION.			
DR	PROSITE; PS00252; INTERFERON_ALPHABETA.			
KFW	CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.			
FT	SIGNAL 1 23			
FT	CHAIN 24 189 INTERFERON ALPHA-6.			
FT	DISULFID 24 122 BY SIMILARITY.			
FT	DISULFID 52 162			
SQ	SEQUENCE 189 AA; 22140 MW; 182468 CN;			
DB	4; Score 1049; Match 86.1%; QryMatch 85.8%; Pred. No. 3.09e-194;			
	Matches 143; Conservative 8; Mismatches 14; Indels 1; Gaps 1;			
Ddb	24 cdlpqthslghrrtmllagmrtrislfscldkdhfrfpqeeqdgngfqkaeisvlhev 83			
Qy				
	1 CDLPQTHSLGSRRTMLLAQMRRISLFSCLIKORDFGFQEEF-GNQFKAETIPVLHEM 59			
Ddb	84 icqtfnlftskdsvawderlldklytelvqglnleacvmqvvggtplmmedsilav 143			
Qy	60 IQQFNLFSTKOSSAAWDETLLDKFYTELTYQQINDLEACVIQGCVGTETPLMKEDSILAV 119			
Ddb	144 rkyfqrilyltkyspcawevrvaeimrfsfssrnqlerlrke 189			
Qy	120 RKYFORITLYKEKKYSPCAWEVRAEIMRSFSLSTNQIESLRKE 165			
RESULT	5			
ID	INA4 HUMAN	STANDARD;	PRT;	189 AA.
AC	P05014; P13358;			
DT	13-AUG-1987 (REL. 05, CREATED)			
DDT	13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)			
DE	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)			
DE	INTERFERON ALPHA-4 PRECURSOR (INTERFERON ALPHA-4B) (INTERFERON ALPHA-M1) (INTERFERON ALPHA-76).			
DGN	INNA4.			
OS	HOMO SAPIENS (HUMAN).			
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;			
OC	EUTHERIA; PRIMATES.			
RN	[1]			
RN	SEQUENCE FROM N.A.			

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GN      IFNAI.4.
SS      HOMO SAPIENS (HUMAN).
CC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
RN      EUROTHERIA; PRIMATES.
[1]
RP      SEQUENCE FROM N.A.
RM      86037205
RR      HENCO K., BROSIUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,
RA      HOCHSTADT J., KOVACIC T., PASEK M., SCHAMBECK A., SCHMID J.,
RAR      TODOKORO K., WAELECHI M., NAGATA S., WEISSMANN C.;
RAN      J. MOL. BIOL. 185:227-260(1985).
[2]
RP      SEQUENCE FROM N.A.
RM      81201124
RR      LAWN R.M., ADELMAN J., DULL T.J., GROSS M., GOEDDEL D.V., ULLRICH A.;
RAL      SCIENCE 212:1159-1162(1981).
[3]
RP      SEQUENCE FROM N.A.
RM      81148795
RR      GOEDEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAWN R.M.,
RAR      MCCANDLISH R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;
RAN      NATURE 290:20-26(1981).
!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
!- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
!- A VARIANT SEQUENCE DIFFERS IN 3 POSITIONS. THE LAST 2 BEING THE
RESULT OF A DELETION FOLLOWED BY AN INSERTION.
EMBL; V00533; HSIFD3.
EMBL; X02959; HSIFNA14.
EMBL; V00542; HSIFR14.
EMBL; J00214; HSIFNAH.
PIR; C23753; IVH014.
HSP; P01563; ZHE.
MM; 147579; 11TH EDITION.
PROSITE; PS00252; INTERFERON_ALPHA.BETA.
CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; GLYCOPROTEIN; SIGNAL.
SIGNAL          1    23
CHAIN           24   189     INTERFERON ALFA-14.
DISULFID        24   122     BY SIMILARITY.
DISULFID        52   162     BY SIMILARITY.
CARBOHYD        25    25     POTENTIAL.
VARIANT         175   175     L -> F.
VARIANT         182   182     Q -> K.
VARIANT         184   184     R -> G.
SEQUENCE       189 AA; 22062 MW; 182495 CN;

DB 4; Score 1050; Match 81.9%; OryMatch 85.9%; Pred. No. 1.88e-194;
Matches 136; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Ddb 24 cnsgethlmrntlmimacmrrispsfcikdchdfefpqeqdgngfqgkagaisvlhem 83
Qy 1 CDLPYSLGSRITLMLLAQMRRISLFCLKDRDDFGFPDEF-GNOFKAEITPVLHEM 59

Ddb 84 mqqfnnlftsnssawdetllekyfielfqcmdleacvlgvgveetplmnedsilav 143
Qy :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
60 IQQIFNLFSKDSSAAWDETLLDKFYELYQLNDLEACVIQGVGVTETPLMKEDSTIAV 119

Ddb 144 kfyqrilylmeqkyspcwewraemrslsfstnlqlrkrd 189
Qy :| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
120 RKYFORITLYIKKKYSPCAWEWRAETMRSFSLTNLSQSIRSKE 165

RESULT 4

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RM 86037205
RA HENCO K., BROSTUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,
RA HOCHSTADT J., KOVACIC T., PASEK M., SCHAMBOECK A., SCHMID J.,
RA TODOKORO K., MAELCHLI M., NAGATA S., WEISSMANN C.;
RL J. MOL. BIOL. 185:227-260(1985).
RN [2]
RP SEQUENCE FROM N.A.
RM 84307815
RA LINNANE A.W., BEILHARZ M.W., MCMULLEN G.L., MACREADIE I.G.,
RA MURPHY M., NISBET I.-I., NOVITSKI C.E., WOODROW G.C.;
RL BIOCHEM. INT. 8:725-732(1984).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; X02955; HSIFNA4B.
DR EMBL; M27318; HSIFNAM1.
DR PIR; E23753; IVH04B.
DR HSP; P01563; ZHIE.
DR MIM; 147564; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON ALPHABETA.
KM CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-4.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 74 74 T -> A (IN REF. 2).
FT CONFLICT 137 137 V -> E (IN REF. 2).
SQ SEQUENCE 189 AA; 21808 MW; 184951 CN;

DB 4; Score 1030; Match 81.3%; QryMatch 84.3%; Pred. No. 4.18e-190;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdipqthslgnrtalillagmrgisfclskdrhdfqfpeefqgkqtaaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTLLMLLAQMRRLISLFCCKDRDRDFGPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqtfnlstedsaaweqsllekfstelyqndleacvigeqvveetplmndvsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYTELYQQLNDLEACVIGQGVGTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsfslsklrlrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKYSPCAWEVVRAEIMRSFSLTNLQESLSRSKE 165

RESULT 6
ID INAK HUMAN STANDARD; PRT; 189 AA.
AC P01568;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-21 PRECURSOR (INTERFERON ALPHA-F) (LEIF F).
GN IFNA21.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 81148795
RA GOEDEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAWN R.M.,
RA MCCANDLISS R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;
RL NATURE 290:20-26(1981).
RN [2]

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RP SEQUENCE FROM N.A.
RA GREN E.Y., BERZIN V.M., TSIMANIS A.Y., APSALON U.R., VISHNEVSKII Y.I.,
RA YANSONE I.V., DISHLER A.V., PUDOVA N.V., SMORODINTSEV A.A.,
RA IOVLEV V.I., STEPANOV A.N., FELDMANE G.Y., MELDRASIS Y.A., LOZHA V.P.,
RA KAVSAN V.M., EFIMOV V.A., SVERDLOV E.D.;
RL DOKL. BIOCHEM. 269:91-95(1983).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; V00540; HSIFR12.
DR EMBL; X00145; HSIFR16.
DR EMBL; J00212; HSIFNAF.
DR PIR; A01832; IVHUF.
DR HSP; P01563; ZHIE.
DR MIM; 147584; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON ALPHABETA.
KM CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-21.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
FT CONFLICT 119 119 M -> L (IN REF. 2).
SQ SEQUENCE 189 AA; 21759 MW; 186062 CN;

DB 4; Score 1027; Match 81.9%; QryMatch 84.0%; Pred. No. 1.88e-189;
Matches 136; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Db 24 cdipqthslgnrtalillagmrgisfclskdrhdfqfpeefqgkqtaaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTLLMLLAQMRRLISLFCCKDRDRDFGPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqtfnlstedsaaweqsllekfstelyqndleacvigeqvveetplmndvsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYTELYQQLNDLEACVIGQGVGTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsfslsklrlrke 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKYSPCAWEVVRAEIMRSFSLTNLQESLSRSKE 165

RESULT 7
ID INAK HUMAN STANDARD; PRT; 189 AA.
AC P01571;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 01-OCT-1994 (REL. 30, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-17 PRECURSOR (INTERFERON ALPHA-I') (INTERFERON
DE ALPHA-T) (INTERFERON ALPHA-88).
GN IFNA17.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 81201124
RA LAWN R.M., ADELMAN J., DULL T.J., GROSS M., GOEDEL D.V., ULLRICH A.;
RL SCIENCE 212:1159-1162(1981).
RN [2]
RP SEQUENCE FROM N.A.
RM 85229953
RA MIZOGUCHI J., PITHA P.M., RAJ N.B.K.;
RL DNA 4:221-232(1985).
RN [3]

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Db	24	cdlptqshlnrralllqamgrispfscldhrhfrfpeeeefghqfqtqtaievlhem	83
Qy	1	CDLPOTHSLGRSRTLLMLLAQMRRIISLFCIKDRDRFCFPQEEF-GNQFKAETIPVLHEM	59
Db	84	iqqtfnlstedsaawegsllkfstelylqqlndleacvicgveetplmedfilav	143
Qy	60	IQQIFNLFSTKDSAAWDETLLDKFYELYQQIANDLEACVIQGVVTEPLMKEDSILAV	119
Db	144	rkvqfritlylmeakyspcawevvraeimrfsfstnlkglrrkd	189
Qy	120	RKYFQRITLYLKEKKYSPCAWEVRAEIMRFSFSLTNLQESLRKSE	165
RESULT 12			
ID	INAI HUMAN	STANDARD;	PRT; 189 AA.
AC	P01562;		
DT	21-JUL-1986	(REL. 01, CREATED)	
DT	21-JUL-1986	(REL. 01, LAST SEQUENCE UPDATE)	
DT	01-FEB-1995	(REL. 31, LAST ANNOTATION UPDATE)	
DE	INTERFERON ALPHA-1/13	PRECURSOR (INTERFERON ALPHA-D) (LEIF D).	
GN	IFNA1 AND IFNA13.		
OS	HOMO SAPIENS (HUMAN).		
OC	EUKARYOTA; METAZOA;	CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;	
OC	EUTHERIA; PRIMATES.		
RP	[1]		
RP	SEQUENCE FROM N.A.		
RM	81005094		
RA	MANTEI N., SCHWARZSTEIN M., STREULI M., PANEM S., NAGATA S.,		
RA	WEISSMANN C.;		
RL	GENE 10:1-10(1980).		
RP	[2]		
RP	SEQUENCE FROM N.A.		
RM	80254543		
RA	TANIGUCHI T., MANTEI N., SCHWARZSTEIN M., NAGATA S., MURAMATSU M.,		
RA	WEISSMANN C.;		
RL	NATURE 285:547-549(1980).		
RP	[3]		
RP	SEQUENCE FROM N.A.		
RM	81148795		
RA	GOSDEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAWN R.M.,		
RA	MCANDLISS R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;		
RL	NATURE 290:20-26(1981).		
RP	[4]		
RP	SEQUENCE FROM N.A.		
RM	8503592		
RA	TODOKORO K., KIOUSSIS D., WEISSMANN C.;		
RL	EMBO J. 3:1809-1812(1984).		
CC	[-]	FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL	
CC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:		
CC	A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.		
CC	[-]	INTERFERONS ALPHA-1 AND ALPHA-13 HAVE IDENTICAL PROTEIN	
CC	SEQUENCES.		
CC	[-]	SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.	
DR	EMBL; V00538; HSIFR10.		
DR	EMBL; X00803; HSIFR18.		
DR	PIR; A01826; IVHUA1.		
DR	PIR; C23285; C23285.		
DR	HSSP; P01563; ZHIE.		
DR	MM; 147578; 11TH EDITION.		
DR	MM; 147660; 11TH EDITION.		
DR	PROSITE; PS00252; INTERFERON ALPHABETA.		
DR	CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.		
FW	SIGNAL		
KT	1	23	

FT	CHAIN	24	189	INTERFERON ALPHA-1/13.
FT	DISULFID	24	122	BY SIMILARITY.
FT	DISULFID	52	162	BY SIMILARITY.
FT	CONFLICT	137	137	A -> V (IN REF. 3).
SQ	SEQUENCE	189 AA;	21725 MW;	177670 CN;
DB	4;	Score	1010;	Match 82.5%; QryMatch 82.7%; Pred. No. 9.25e-186;
	Matches	137;	Conservative	13; Mismatches 15; Indels 1; Gaps 1;
Db	24	cdlpethelndrrtlllqgmrrispsckldrhdffpqqefdnqfqpaisvhl	83	
Qy	1	CDLPQTHSLGSRRTLLLAQMRRIISLFSCLKDRDFFGPQEEF-GNQFQKAETIPVLHEM	59	
Db	84	iqqifnlftkdsaaawdelldkftelylqqlndleacvmqgeervgetplmndsilav	143	
Qy	60	IQQIFNLFTKDSAAWDELTDLDFYELYLQQLNDLEACVIQGVGVETPTLMKEDSILAV	119	
Db	144	kyfrtityltekyspcawevraeirmslsltnqlrrke	189	
Qy	120	KYFQRITLYLKEKYSPCAWEVRAEIRMSFSLTNQESLRKE	165	
RESULT	13			
ID	IN44_HORSE	STANDARD;	PRT;	184 AA.
AC	P05006;			
DT	13-AUG-1987	(REL. 05, CREATED)		
DT	13-AUG-1987	(REL. 05, LAST SEQUENCE UPDATE)		
DT	01-MAR-1989	(REL. 10, LAST ANNOTATION UPDATE)		
DE	INTERFERON ALPHA-4	PRECURSOR.		
OS	EQUUS CABALLUS	(HORSE).		
OC	EUKARYOTA;	METAZOA;	CHORDATA;	VERTEBRATA; TETRAPODA; MAMMALIA;
OC	EUTHERIA;	PERISSODACTYLA.		
RN	[1]			
RM	SEQUENCE FROM N.A.			
RP	87053170			
RA	HIMMLER A., HAUPTMANN R., ADOLF G.R., SWETLY P.;			
RL	DNA 5:345-356 (1986).			
CC	-!- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL			
CC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:			
CC	A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.			
CC	-!- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.			
DR	EMBL; M14543; ECIFN4A.			
DR	PIR; D24912; IVH04A.			
DR	HSSP; P01563; ZHIE.			
DR	PROSITE; PS00252; INTERFERON ALPHABETA.			
DR	CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.			
KW	SIGNAL	1 23		
FT	CHAIN	24	184	INTERFERON ALPHA-4.
FT	DISULFID	24	122	BY SIMILARITY.
FT	DISULFID	52	162	BY SIMILARITY.
SQ	SEQUENCE	184 AA;	20860 MW;	178676 CN;
DB	4;	Score	953;	Match 77.0%; QryMatch 78.0%; Pred. No. 2.13e-173;
	Matches	124;	Conservative	19; Mismatches 17; Indels 1; Gaps 1;
Db	24	cdlpethelngtrvmlqgmrrispsckldrhdffpqqefdnqfqpaisavhet	83	
Qy	1	CDLPQTHSLGSRRTLLLAQMRRIISLFSCLKDRDFFGPQEEF-GNQFQKAETIPVLHEM	59	
Db	84	iqqifnlftkdsaaawdelldklytglylqqlndleacslsqveevetplmndsilav	143	
Qy	60	IQQIFNLFTKDSAAWDELTDLDFYELYLQQLNDLEACVIQGVGVETPTLMKEDSILAV	119	
Db	144	rryfrtitylqekyspcawevraeirmsfssstnlpq	184	

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QY      120 RKYFORITLYKEKKYSPCAWEVVRIMRFSLSLNLQES 160
       :|:||||||| | |||||:||||||| ||| :|
RESULT  14
ID      INA2 HORSE          STANDARD;          PRT;    184 AA.
AC      P05004;
DT      13-AUG-1987 (REL. 05, CREATED)
DT      13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT      01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
DE      INTERFERON ALPHA-2 PRECURSOR.
OS      EQUUS CABALLUS (HORSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PERISSODACTYLIA.
RN      (1)
RN      SEQUENCE FROM N.A.
RM      87053170
RA      HIMMLER A., HAUPTMANN R., ADOLF G.R., SWETLY P.;
RL      DNA 5:345-356(1986).
CC      -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC      ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC      A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC      -I- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR      EMBL; M14541; ECIFN2.
DR      PIR; B24912; IVHOA2.
DR      HSPP; P01563; ZHIE.
DR      PROSITE; PS00252; INTERFERON ALPHABETA.
DR      CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
KT      SIGNAL 1 23
FT      CHAIN 24 184 INTERFERON ALPHA-2.
FT      DISULFID 24 122 BY SIMILARITY.
FT      DISULFID 52 162 BY SIMILARITY.
SQ      SEQUENCE 184 AA; 20877 MW; 172708 CN;

DB 4; Score 952; Match 76.4%; QryMatch 77.9%; Pred. No. 3.50e-17
Matches 123; Conservative 20; Mismatches 17; Indels 1; Gaps

Db      24 cdlphthalgntrivmlgmgmrissfclskdrndfqbgvdfqngcfkpgaisavhet 83
       |||||:||||| 1 |||||:||||| ||||| ||||| |||||:|||||: ||
QY      1 CDLPHTSLGSRRTLMLLAQMRRIISLFCLKDRDRDFGPPEEF-GNQFOKAETIPVLHEM 59
       |||||:||||| 1 |||||:||||| ||||| ||||| |||||:|||||: ||
Db      84 iqquihlfstgssaaawdeslldklytglycqlteleacisqevgvveetplmnedslilav 143
       |||||:||||| 1 |||||:||||| ||||| ||||| |||||:|||||: ||
QY      60 IQQIFNFSTKDSAAWDETLLDKFEYTYQLNDLEACVIQGVGVTETPLMKEDSLAV 119
       |||||:||||| 1 |||||:||||| ||||| ||||| |||||:|||||: ||
Db      144 rryfricrllyqekkyscaweivraeimrcfsastnlqqss 184
       |:|||||:||||| 1 |||||:||||| ||||| ||||| |||||:|||||: ||
QY      120 RKYFORITLYKEKKYSPCAWEVVRIMRFSLSLNLQES 160
       :|:||||||| | |||||:||||||| ||| :|
RESULT  15
ID      INA1 HORSE          STANDARD;          PRT;    184 AA.
AC      P05003;
DT      13-AUG-1987 (REL. 05, CREATED)
DT      13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT      01-MAR-1989 (REL. 10, LAST ANNOTATION UPDATE)
DE      INTERFERON ALPHA-1 PRECURSOR.
OS      EQUUS CABALLUS (HORSE).
OC      EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC      EUTHERIA; PERISSODACTYLIA.
RN      (1)
RN      SEQUENCE FROM N.A.
RM      87053170
RA      HIMMLER A., HAUPTMANN R., ADOLF G.R., SWETLY P.;

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RL DNA 5:345-356(1986).
CC -I- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC - A PROTEIN KINASE AND AN OLIGOMENYLATED SYNTHETASE.
CC -I- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
CC EMBL: M14540; ECIEFNA.
DR PIR: A24912; IYHOAL.
DR HSSP: P01563; ZHIE.
DR PROSITE: PS00252; INTERFERON ALPHABETA.
KW CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 184 INTERFERON ALPHA-1.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 184 AA; 20808 MW; 176176 CN;

DB 4; Score 950; Match 76.4%; QryMatch 77.7%; Pred. No. 9.49e-173;
Matches 123; Conservative 20; Mismatches 17; Indels 1; Gaps 1;

Db 24 cdplphthelgntrvlmlgqmrispsclkrndrfgqevfdngnfrkbpqaisavhet 83
||||:||||:| ||||:||||:||||:||||:||||:||||:||||:||||: |||
Qy 1 CDLPQTHSLGSRRTLMILAQMRRISLFSCLKDRDFGFPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqlfhlfstgsgaawdeslldklytglyqglteleaclsgqvgeetplmmedsllav 143
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: |||
Qy 60 IQQINFSTKDSAAWDETLLDKFTLYLYQLQNDLEACVIQGVGVTEPTLMKEDSILAV 119

Db 144 ryrfqrialyqkksycspcaweivraeimrfsfstnlpqgs 184
||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||: |||
Qy 120 RYFQRITLYLKEKKYSPCAWEVVRAEIMRFSFSLSTNLQES 160

Search completed: Tue Aug 29 17:04:28 1995
Job time : 12 secs.

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CC The glycosylated IFN's is used (partic. in a mixt. of at least
 CC 2 of the alpha-2a, -2b or -2c forms) for treatment of viral and
 CC tumour diseases.
 CC See also Q20731-43 and Q20522-26.
 SQ Sequence 188 AA;

DB 4; Score 1222; Match 100.0%; QryMatch 100.0%; Pred. No. 1.34e-103;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdldpqlhslgrrtllmlagmrriisfclskdrdrdfgfpgeefgnqfkaetipvlhemi 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1 CDLPQTHSLGSRRTLLMLAQMRRIISFLSCLKDRDRDFGFPQEEFGNQFKAETIPVLHEMI 60

Db 84 qqifnlfstkdsaaawdetlldkfytelqqindleacviggvgtetplmkedsilavr 143
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGGVGTETPLMKEDSILAVR 120

Db 144 kyfqrtilylkekyspcawevvraeimrfsfstlnqlsrske 188
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSFSSTLNQLSRSKE 165

RESULT 2

ID R20549 standard; Protein; 188 AA.

AC R20549;

DT 21-APR-1992 (first entry)

DE Human IFNalpha 2C from pAD19b-IFN.

KW Interferon; O-glycosylation.

OS Homo sapiens.

FH Key Location/Qualifiers

FT Peptide 1..23

FT /label= sig_peptide

FT Protein 24..188

FT /label= mat_protein

PN DE4021917-A.

PD 16-JAN-1992.

PF 10-JUL-1990; 021917.

PR 10-JUL-1990; DE-021917.

PA (BOEH) BOEHRINGER INGELHEIM.

PI Hummler A, Adolf G;

DR WPI; 92-025485/04.

DR N-PSDB; Q20764.

PT O-glycosylated alpha-interferon, used as medicament - isolated

PT following secretion into conditioned medium of mammalian cells

PT contg. a suitable expression plasmid

PS Disclosure; Fig 6; 24pp; German.

CC Human embryonic kidney cells transformed with the human IFNalpha

CC 2C gene, contd. in pAD19b-IFN, are grown under suitable conditions.

CC O-glycosylated IFNalpha can then be isolated and purified from the

CC tissue culture supernatant.

CC See also Q20764-66 and Q22517-29.

SQ Sequence 188 AA;

DB 3; Score 1222; Match 100.0%; QryMatch 100.0%; Pred. No. 1.34e-103;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdldpqlhslgrrtllmlagmrriisfclskdrdrdfgfpgeefgnqfkaetipvlhemi 83
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1 CDLPQTHSLGSRRTLLMLAQMRRIISFLSCLKDRDRDFGFPQEEFGNQFKAETIPVLHEMI 60

Db 84 qqifnlfstkdsaaawdetlldkfytelqqindleacviggvgtetplmkedsilavr 143
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGGVGTETPLMKEDSILAVR 120

Db 144 kyfqrtilylkekyspcawevvraeimrfsfstlnqlsrske 188
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSFSSTLNQLSRSKE 165

RESULT 3

ID P70329 standard; Protein; 166 AA.

AC P70329;

DT 20-MAY-1991 (first entry)

DE Sequence of IFN-alpha-2 (Arg).

KW Hybrid alpha/omega interferon; antiviral; virucide; antitumour;

KW cytostatic.

PN EP-236920-A.

PD 16-SEP-1987.

PF 04-MAR-1987; 103030.

PR 10-MAR-1986; DE-607835.

PA (BOEH) BOEHRINGER INGELHEIM.

PI Hauptmann R, Swetly P, Meindl P, Gunther A, Falkner E,

PI Bodo G, Maurer-Fogy I;

DR WPI; 87-258223/37.

DR N-PSDB; N70528.

PT New hybrid interferon prods. useful as antiviral agents - contg.

PT alpha and omega interferon fragments

PS Disclosure; pp4-6; 65pp; German.

CC Hybrid interferons comprising a fragment of an alpha-interferon and

CC a fragment of an omega-interferon, and their N-terminal Met or

CC N-formyl-Met derivs. and N-glycosylated derivs., are new. The hybrid

CC interferons are useful as antiviral and antitumour agents. Both IFN-

CC alpha-2(Arg) and omega-1-interferon has a 191-196 BglII restriction

CC site (see N70528 and N70529). In addition, IFN-alpha-2(Arg) has a

CC 451-456 BglII site.

SQ Sequence 166 AA;

DB 2; Score 1222; Match 100.0%; QryMatch 100.0%; Pred. No. 1.34e-103;
 Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdldpqlhslgrrtllmlagmrriisfclskdrdrdfgfpgeefgnqfkaetipvlhemi 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 1 CDLPQTHSLGSRRTLLMLAQMRRIISFLSCLKDRDRDFGFPQEEFGNQFKAETIPVLHEMI 60

Db 62 qqifnlfstkdsaaawdetlldkfytelqqindleacviggvgtetplmkedsilavr 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGGVGTETPLMKEDSILAVR 120

Db 122 kyfqrtilylkekyspcawevvraeimrfsfstlnqlsrske 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSFSSTLNQLSRSKE 165

RESULT 4

ID P50228 standard; Protein; 165 AA.

AC P50228;

DT 24-NOV-1991 (first entry)

DE Interferon alpha-2.

KW Interferon alpha-2; hybrid protein; crossover region.

FH Key Location/Qualifiers

FT Region 62..65

FT /label= crossover region A

FT Region 87..94

FT /label= crossover region B

FT Region 87..100

FT /label= crossover region C

FT Region 87..105

FT /label= crossover region D

FT Region 108..112
 FT /label= crossover region E
 FT Region 113..116
 FT /label= crossover region F
 FT Region 125..130
 FT /label= crossover region G
 FT Region 132..150
 FT /label= crossover region H
 FT Region 152..153
 FT /label= crossover region I
 FT Region 154..160
 FT /label= crossover region J
 FT Region
 PN EP-14184-A.
 PD 15-MAY-1985.
 PF 05-JUN-1984; 303787.
 PR 10-JUN-1983; GB-015980.
 PA (BIOJ) Biogen NV.
 PI Weismann C, Weber H.
 DR WPI; 85-117654/20.
 DR N-PSDB; N50272.
 PT New hybrid DNA sequences and hybrid polypeptide(s) - useful in prodn.
 PT of interferon(s), lymphokines, viral antigens, etc.
 PS Disclosure; Fig. 6A-C; 47pp; English.
 CC The DNA encoding interferon alpha-2 may be fused to a second
 CC coding sequence, eg for animal or human alpha, beta or gamma-
 CC interferons, lymphokines, foot-and-mouth disease antigens, to form a
 CC hybrid DNA. The DNA must be fused to the second DNA sequence in the
 CC same reading frame to maintain a constant reading frame through a
 CC crossover region common to both sequences. The hybrid restriction sites
 CC obd. without the need for chance availability of restriction sites
 CC to be combined. Sequential deletions to give prods. with modified
 CC properties, activity and specificity are reliable.
 SQ Sequence 165 AA;
 DB 3; Score 1215; Match 99.4%; QryMatch 99.4%; Pred. No. 6,27e-103;
 Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 cdipqthslgsrrtlmllagmrriisfscldkrdhdfgfpqeeefgnqfkaetipvlhemi 60
 Qy 1 CDLPQTHSLGSRRTLMLLAQMRRIISFSLCKDRDFGFPQEEFGNQFQKAETIPVLHEMI 60
 Db 61 qqifnlfstkdsaaawdetllldkfytellyqqlndleacvlgvgvgtetplmkedsilavr 120
 Qy 61 QQIFNLFSKDSAAWDETLLDKFYTELYQQQLNDLEACVIGVGVTETPLMKEDSILAVR 120
 Db 121 kyfqrtillykkykspcawevvraeimrfsfsltnlqeslrsk 165
 Qy 121 KYFQRITLYLKKYKSPCAMEVVRAEIMRFSFSLTNLQESLSRKE 165
 DB 3; Score 1215; Match 99.4%; QryMatch 99.4%; Pred. No. 6,27e-103;
 Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 1 cdipqthslgsrrtlmllagmrriisfscldkrdhdfgfpqeeefgnqfkaetipvlhemi 60
 Qy 1 CDLPQTHSLGSRRTLMLLAQMRRIISFSLCKDRDFGFPQEEFGNQFQKAETIPVLHEMI 60
 Db 61 qqifnlfstkdsaaawdetllldkfytellyqqlndleacvlgvgvgtetplmkedsilavr 120
 Qy 61 QQIFNLFSKDSAAWDETLLDKFYTELYQQQLNDLEACVIGVGVTETPLMKEDSILAVR 120
 Db 121 kyfqrtillykkykspcawevvraeimrfsfsltnlqeslrsk 165
 Qy 121 KYFQRITLYLKKYKSPCAMEVVRAEIMRFSFSLTNLQESLSRKE 165
 RESULT 5
 ID P20114 standard; Protein; 166 AA.
 AC P20114;
 DT 21-SEP-1992 (first entry)
 DE Human interferon-alpha-2.
 KW Interferon-alpha-2.
 OS Synthetic.
 PN EP-62971-A.
 PD 20-OCT-1982.
 PF 15-MAR-1982; 301309.
 PR 27-MAR-1981; GB-009678.
 PR 30-MAR-1981; GB-009919.
 PR 22-APR-1981; GB-012446.

PR 07-SEP-1981; GB-026979.
 PA (ICIL) IMPERIAL CHEM INDOS PLC.
 PA (UYLE-) UNIV OF LEICESTER.
 PI Atherton KT, DeMaeyer E, Edge MD, Markham AF, Meacock PA;
 PI Windass JD.
 DR WPI; 82-90772E/43 (90772E).
 DR N-PSDB; N20109.
 PT Genetically modified microorganisms - capable of expressing as
 PT metabolite a cpd. having interferon activity.
 PS Disclosure; Fig 2; 70pp; English.
 CC Interferon may be expressed from a synthetic gene and may be used
 CC as a virucide and antitumor agent or as an immunostimulant.
 SQ Sequence 166 AA;
 DB 5; Score 1215; Match 99.4%; QryMatch 99.4%; Pred. No. 6,27e-103;
 Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Db 2 cdipqthslgsrrtlmllagmrriisfscldkrdhdfgfpqeeefgnqfkaetipvlhemi 61
 Qy 1 CDLPQTHSLGSRRTLMLLAQMRRIISFSLCKDRDFGFPQEEFGNQFQKAETIPVLHEMI 60
 Db 62 qqifnlfstkdsaaawdetllldkfytellyqqlndleacvlgvgvgtetplmkedsilavr 121
 Qy 61 QQIFNLFSKDSAAWDETLLDKFYTELYQQQLNDLEACVIGVGVTETPLMKEDSILAVR 120
 Db 122 kyfqrtillykkykspcawevvraeimrfsfsltnlqeslrsk 166
 Qy 121 KYFQRITLYLKKYKSPCAMEVVRAEIMRFSFSLTNLQESLSRKE 165
 RESULT 6
 ID P10018 standard; Protein; 182 AA.
 AC P10018;
 DT 13-AUG-1992 (first entry)
 DE Sequence of interferon (IFN) -alpha-2 encoded by the Hif-II-206
 DE fragment of culture HcIF-G.
 KW Anti-viral agent; anti-cancer agent; therapy; tumour.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT Peptide 1..17
 PN EP-32134-A.
 PD 15-JUL-1981.
 PF 07-JAN-1981; 300050.
 PR 08-JAN-1980; EP-300079.
 PR 03-APR-1980; EP-301100.
 PR 02-OCT-1980; GB-031737.
 PA (BIOJ) BIOGEN NV.
 PI Weismann C;
 DR WPI; 81-53697D/30.
 DR N-PSDB; N10011.
 PT DNA sequences coding for interferon-like polypeptide(s) - useful
 PT as antiviral or antitumour agents
 PS Claim 22; Fig 12-16; 136pp; English.
 CC The inventors claim DNA sequences coding for interferon-like
 CC polypeptide(s). The DNA sequences pref. encode IFN-alpha type 1, 2,
 CC 4a and 4b. Pref. DNA sequences which hybridise to the inserts of 2-
 CC pBR322(Pst)/HcIF-4c, 2-pBR322(Pst)/HcIF-2h, 2-pBR322(Pst)/HcIF-SN35,
 CC 2-pBR322(Pst)/HcIF-SN42 and 2pKT287(Pst)/HcIF-2h-AH6 comprise
 CC 2-pBR322(Pst)/HcIF-II-206, 2-pBR322(Pst)/HcIF-SN35-AHL6, and
 CC Hif-chrl, -3, -12, -13, -16-1, -26, -30, -35, -19 and -27. Pref.
 CC recombinant DNA molecules are C8-IFN-alpha-1, C8-IFN-alpha-2,
 CC IAC-AUG(alpha-2) and beta-lac-AUG(alpha-2). A comparison of the
 CC nucleotide sequence of the coding region of HcHIF-35H8-alpha and
 CC that of Hif-2h (coding region) reveals that they are identical.

SQ Sequence 182 AA;

DB 4; Score 1215; Match 99.4%; QryMatch 99.4%; Pred. No. 6.27e-103; Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 18 cdlpqtshlgsrrtllmllagmrriisfclckdrhdfgfpqeeqngfqkaetipvlhemi 77
 QY 1 CDLPQTHSLGSRRTLLMLLAQMRRIISFCLCKDRDRDFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 78 qqifnlfdksaaawdetllldkfytelyqqldndleacviggvgtetplmkedsilavr 137
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGGVGTETPLMKEDSILAVR 120

Db 138 kyfqrtilylkekyspcawevvraeimrfsfstnlqeslrsk 182
 QY 121 KYFQRITLYLKEKKYSPCAWEVVRAEIMRFSFSLTNLQESLSRKE 165

RESULT 7

ID P60037 standard; Protein; 166 AA.

AC P60037;

DT 31-JUL-1991 (first entry)

DE Sequence encoded by synthetic human interferon-alpha 2

DE (hIFN-alpha-2) gene

KW Antiviral; interferon purification.

OS Homo sapiens.

PN EP-194006-A.

PD 10-SEP-1986.

PF 17-JAN-1986; 300304.

PR 01-FEB-1985; GB-002605.

PR 25-JUN-1985; US-748558.

PA (ICIL) IMPERIAL CHEM INDUS PLC.

PI Camble R, Edge MD;

DR WPI; 86-240111/37.

DR N-PSDB; N60045.

PT New polypeptide analogues of human interferon alpha2 - with high antiviral activity, and DNA coding sequences

PS Disclosure; Figure 1; 78pp; English.

CC 8 cpds. are specifically claimed, e.g. IFN-alpha2 (4-155); (Leu-59)-IFN-alpha2 or (Ser-29, 138)-IFN-alpha2

SQ Sequence 166 AA;

DB 3; Score 1215; Match 99.4%; QryMatch 99.4%; Pred. No. 6.27e-103; Matches 164; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdlpqtshlgsrrtllmllagmrriisfclckdrhdfgfpqeeqngfqkaetipvlhemi 61
 QY 1 CDLPQTHSLGSRRTLLMLLAQMRRIISFCLCKDRDRDFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 62 qqifnlfdksaaawdetllldkfytelyqqldndleacviggvgtetplmkedsilavr 121
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGGVGTETPLMKEDSILAVR 120

Db 122 kyfqrtilylkekyspcawevvraeimrfsfstnlqeslrsk 166
 QY 121 KYFQRITLYLKEKKYSPCAWEVVRAEIMRFSFSLTNLQESLSRKE 165

RESULT 8

ID P30163 standard; peptide; 175 AA.

AC P30163;

DT 14-JUN-1992 (first entry)

DE Sequence encoded by a modified BamHI human interferon-alpha gene fragment.

KW Yeast expression vector; Saccharomyces cerevisiae; promoter;

OS glycolytic enzyme; phosphoglycerate kinase.

PN EP-73635-A.

PD 09-MAR-1983.

PF 17-AUG-1982; 408826.

PR 25-AUG-1981; GB-025934.

PR 23-MAR-1982; GB-008422.

PR 16-JUN-1982; GB-017496.

PA (KING/) KINGSMAN A J.

PA (CELL-) CELLSMAN A J.

PI Kingsman S M; Kingsman A J.

DR WPI; 83-25586K/11.

DR N-PSDB; N30062.

PT Yeast expression vector for transforming yeasts - useful in economic prodn. of polypeptide(s) esp. human interferon-alpha Example; Fig 16; 45pp; English.

CC The inventors claim a yeast expression vector comprising a yeast selective marker, a yeast replication origin and a yeast promoter positioned relative to a unique restriction site. The yeast CC coding for glycolytic enzyme, esp. of the yeast PCK gene located upstream of the unique restriction site and at least part of the 3' CC region of the PCK gene located downstream of the site. The vector CC is used to express a polypeptide, eg. human interferon-alpha.

SQ Sequence 175 AA;

DB 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 1.88e-102; Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 11 cdlpqtshlgsrrtllmllagmrriisfclckdrhdfgfpqeeqngfqkaetipvlhemi 70
 QY 1 CDLPQTHSLGSRRTLLMLLAQMRRIISFCLCKDRDRDFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 71 qqifnlfdksaaawdetllldkfytelyqqldndleacviggvgtetplmkedsilavr 130
 QY 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGGVGTETPLMKEDSILAVR 120

Db 131 kyfqrtilylkekyspcawevvraeimrfsfstnlqeslrsk 175
 QY 121 KYFQRITLYLKEKKYSPCAWEVVRAEIMRFSFSLTNLQESLSRKE 165

RESULT 9

ID P40022 standard; Protein; 166 AA.

AC P40022;

DT 30-NOV-1991 (first entry)

DE Recombinant interferon-alpha A.

KW Recombinant interferon-alpha A; antiviral.

PN EP-128467-A.

PD 19-DEC-1984.

PF 30-MAY-1984; 106214.

PR 01-JUN-1983; US-499964.

PA (HOFF) F Hoffmann-La Roche & Co.

PI DeChiara TM, Tarnowski SJ Jr.

DR WPI; 84-313909/51.

DR N-PSDB; N40013.

PT New antiviral interferon polypeptide(s) free from oligomers - with cysteine residues replaced by other amino acid residues.

PS Disclosure; Fig. 1; 46pp; English.

CC The protein is recombinant interferon-alpha A (rIFN aa). The CC fragment comprising amino acids 3-166 is claimed. In this CC protein, Cys 1 may be replaced by a glycine residue, and Cys 98, CC 99 or 100 may be replaced by Ser. These polypeptides have antiviral

CC activity, but unlike prior interferons they are free from
 CC oligomers, other than dimers, and they pref. consist of stable
 CC monomers only.
 SQ Sequence 166 AA;

DB 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 1.88e-102;
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdllpghslgsrrtllmllagmrkislfcslkdrhdgfpgeefgnqfkaetipvlhemi 61
 |||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCIKDRRDFGFPQEEFCNQFQKAETIPVLHEMI 60

Db 62 qqifnlfstkdsaaawdetlldkfytelylqqldndleacvlgvgvgtetplmkedsilavr 121
 |||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGVGVTETPLMKEDSILAVR 120

Db 122 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrake 166
 |||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLSTNLQESLSRKE 165

RESULT 10
 ID R05400 standard; protein; 182 AA.

AC R05400;
 DT 11-OCT-1990 (first entry)
 DE Hybrid Hu-IFN alpha A/gamma.
 KW Hu-IFN; interferon; tumour; cancer; ds.
 OS Homo sapiens.
 PN EP-372707-A.
 PD 13-JUN-1990.
 PF 27-OCT-1989; 311108.
 PR 28-OCT-1988; US-264271.
 PA (PEST/) Pestka S.
 PI Pestka S;
 DR WPI; 90-180507/24.
 DR N-PSDB; Q04744.
 PT Phosphorylated modified proteins, including modified interferon(s) -
 PT used in diagnostic and therapeutic applications. eg.
 PT pharmacokinetic studies and tumour treatment.
 PS Claim 8; Fig 3; 47pp; English.
 CC Hybrid IFN-gamma and IFN-alpha can be phosphorylated to a high
 CC radio specific activity which IFN-alpha alone cannot.
 CC By introducing phosphorylatable groups, the proteins may be used in
 CC pharmacokinetic studies and diagnostic applications, by attaching 32P
 CC labels to the incorporated sites.
 SQ Sequence 182 AA;

DB 1; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 1.88e-102;
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdllpghslgsrrtllmllagmrkislfcslkdrhdgfpgeefgnqfkaetipvlhemi 61
 |||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCIKDRRDFGFPQEEFCNQFQKAETIPVLHEMI 60

Db 62 qqifnlfstkdsaaawdetlldkfytelylqqldndleacvlgvgvgtetplmkedsilavr 121
 |||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGVGVTETPLMKEDSILAVR 120

Db 122 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrake 166
 |||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLSTNLQESLSRKE 165

RESULT 11

ID P20103 standard; Protein; 188 AA.
 AC P20103;
 DT 10-AUG-1992 (first entry)
 DE Sequence encoded by leukocyte interferon LeIF A cDNA.
 KW Viral infection; therapy; malignancy.
 OS Homo sapiens.
 FH Key Location/Qualifiers

FT Peptide
 FT /label= signal
 PN CB2079291-A.
 PD 20-JAN-1982.

PF 01-JUL-1981; 120279.
 PR 01-JUL-1980; US-164986.
 PR 08-SEP-1980; US-184909.
 PR 10-NOV-1980; US-205578.

PR 21-APR-1981; US-256204.
 PA (HOFF) HOFFMANN-LA ROCHE AG.
 PA (GENE-) GENENTECH INC.
 PI Goeddel DYN, Pestka S;
 DR WPI; 82-04460E/03.

DR N-PSDB; N20090.
 PT Mature human leukocyte interferon polypeptide(s) - prepd. from
 PT microbes transformed with appropriate DNA sequences

PS Disclosure; Fig 4; 20pp; English.
 CC The inventors claim a polypeptide comprising the AA sequence of a
 CC mature human LeIF and a DNA sequence encoding it. LeIF A-D, F, H-J
 CC and encoding DNA are specifically claimed. They are natural allelic
 CC variations. LeIF is isolated from the leukocytes of humans with
 CC chronic myelogenous leukaemia, induced to produce interferon with
 CC Sendai or Newcastle disease virus; esp. the cell line KG-1.
 SQ Sequence 188 AA;

DB 5; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 1.88e-102;
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdllpghslgsrrtllmllagmrkislfcslkdrhdgfpgeefgnqfkaetipvlhemi 83
 |||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCIKDRRDFGFPQEEFCNQFQKAETIPVLHEMI 60

Db 84 qqifnlfstkdsaaawdetlldkfytelylqqldndleacvlgvgvgtetplmkedsilavr 143
 |||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQLDNDLEACVIGVGVTETPLMKEDSILAVR 120

Db 144 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrake 188
 |||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLSTNLQESLSRKE 165

RESULT 12

ID R38793 standard; Protein; 216 AA.

AC R38793;
 DT 21-JAN-1994 (first entry)

DE Natural human interferon-alpha.
 KW IFN-alpha; hIFN-alpha.

OS Homo sapiens.
 FH Key Location/Qualifiers

FT Region 26
 FT /note= "Natural mature human alpha-interferon N-terminal"

FT Region 190
 FT /note= "Natural mature human alpha-interferon C-terminal"

FT Region 191
 FT /note= "corresponds to termination codon"

FT Region 211
 FT /note= "corresponds to termination codon"

PN EP-553494-A.
 PD 04-AUG-1993.
 PF 29-DEC-1992; 122084.
 PR 31-DEC-1991; KR-025878.
 PR 31-DEC-1991; KR-025879.
 PR 28-JAN-1992; KR-001155.
 PA (LUCK-) LUCKY LTD.
 PI Bae TO, Chang HJ, Cho JM, Park SJ, Park YW.
 DR WPI; 93-244548/31.
 DR N-PSDB; Q47153.
 PT Recombinant human alpha interferon and corresp. gene - for
 PT efficient expression in yeast, and purificn. process
 PS Disclosure; Fig 1B; 30pp; English.
 CC The sequence is that of natural human interferon-alpha.
 SQ Sequence 216 AA;

DB 7; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 1.88e-102;
 Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 26 cdlpcthslgrrtllmllagmrkislfcslkdrhdfgfpqeeqngqkaetipvlhemi 85
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCISKDRDRFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 86 qqifnlfstkdsaaawdetlldkfytelyqqindleacvlgvgvtetplmkedsilavr 145
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGVGVTETPLMKEDSILAVR 120

Db 146 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrsk 190
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLTNLQESLSRKE 165

RESULT 13
 ID P70327 standard; protein; 165 AA.
 AC P70327;
 DT 06-FEB-1991 (first entry)
 DE Recombinant alpha-2 interferon analogue.
 KW Alpha-interferon analogue; proteolysis resistance; IFN
 FH Key Location/Qualifiers
 FT Misc difference 22..22
 FT /Label= T, S, N, Q, G
 PN EP-240224-A.
 PD 07-OCT-1987.
 PF 24-MAR-1987; 302519.
 PR 31-MAR-1987; US-845937.
 PA (INTE) Interferon Sci Inc.
 PI O'Loughlin J T
 DR WPI; 87-279540/40.
 PT New active alpha-interferon analogues resistant to proteolysis - at
 PT positions 22 and 23, which are expressed intact in host cells,
 PT especially Saccaromyces cerevisiae.
 PS Disclosure; Fig. 2; 20pp; English.
 CC The recombinant alpha-interferon analogue lacks the dibasic
 CC diaminopeptidase recognition site at positions 22 and 23 which are
 CC present in native alpha-IFN, while still retaining alpha-IFN activity.
 CC Oligonucleotides are used to direct mutagenesis.
 SQ Sequence 165 AA;

DB 2; Score 1206; Match 98.8%; QryMatch 98.7%; Pred. No. 4.54e-102;
 Matches 163; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 1 cdlpcthslgrrtllmllagmrkislfcslkdrhdfgfpqeeqngqkaetipvlhemi 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCISKDRDRFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 61 qqifnlfstkdsaaawdetlldkfytelyqqindleacvlgvgvtetplmkedsilavr 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGVGVTETPLMKEDSILAVR 120

Db 121 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrsk 165
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLTNLQESLSRKE 165

RESULT 14
 ID R38792 standard; Protein; 166 AA.
 AC R38792;
 DT 21-JAN-1994 (first entry)
 DE Recombinant human alpha Interferon.
 KW Yeast-preferred codons; efficient expression; high yield;
 KW IFN-alpha.
 OS Homo sapiens.
 PN EP-553494-A.
 PD 04-AUG-1993.
 PF 29-DEC-1992; 122084.
 PR 31-DEC-1991; KR-025878.
 PR 31-DEC-1991; KR-025879.
 PR 28-JAN-1992; KR-001155.
 PA (LUCK-) LUCKY LTD.
 PI Bae TO, Chang HJ, Cho JM, Park SJ, Park YW.
 DR WPI; 93-244548/31.
 DR N-PSDB; Q47152.
 PT Recombinant human alpha interferon and corresp. gene - for
 PT efficient expression in yeast, and purificn. process
 PS Claim 9; Fig 1A; 30pp; English.
 CC The sequence is that encoded by a recombinant human alpha-interferon
 CC gene which was designed to have yeast-preferred codons and to minimise
 CC the formation of mRNA secondary structure, so that transcription
 CC and translation efficiency is increased. This enables efficient
 CC expression in yeast of the alpha-interferon.
 SQ Sequence 166 AA;

DB 7; Score 1205; Match 98.2%; QryMatch 98.6%; Pred. No. 5.66e-102;
 Matches 162; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdlpcthslgrrtllmllagmrkislfcslkdrhdfgfpqeeqngqkaetipvlhemi 61
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFCISKDRDRFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 62 qqifnlfstkdsaaawdetlldkfytelyqqindleacvlgvgvtetplmkedsilavr 121
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 QQIFNLFSTKDSAAWDETLLDKFYTELYQQINDLEACVIGVGVTETPLMKEDSILAVR 120

Db 122 kyfqrtilylkekyspcawevvraeimrfsisltnlqeslrsk 166
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRFSISLTNLQESLSRKE 165

RESULT 15
 ID P60119 standard; protein; 164 AA.
 AC P60119;
 DT 10-JUN-1991 (first entry)
 DE Interferon-gamma.
 KW Interferon-gamma; virucide; antitumor.
 FH Key Location/Qualifiers
 FT Disulfide-bond 1..98
 FT Disulfide-bond 29..138
 PN EP-203382-A.

PD 03-DEC-1986.
PF 25-APR-1986; 105722.
PR 27-APR-1985; DE-515336.
PA (BOEH) BOEHRINGER INGELHEIM.
PI Bodo G, Maurer-Fogy I, Falkner E, Linder SJ.
DR WPI; 86-320384/49.
PT High purity, non immunogenic recombinant alpha interferon prodn.
PT - by harvesting cells as specific growth stage, protein extn. and
PT three stage chromatography purificn.
PS Claim 1; Page 20; 33pp; Ge.
CC The recombinant protein is expressed in E. coli, and is useful for
CC treating virus infections and tumours.
SQ Sequence 164 AA,

DB 2; Score 1204; Match 99.4%; QryMatch 98.5%; Pred. No. 7.06e-102;
Matches 164; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Db 1 cdipqthslgsrrtllmllagmrriisfscldkrrdfgpggeefgnqgkaetipvlhemi 60
|||||
Qy 1 CDLPQTHSLGSRRTLLMLAQMRRIISLFSCLKDRRDFGPPQEEFGNQFQKAETIPVLHEMI 60

Db 61 qqifnlfsdkdsaaawdetllldkfytelyqqldleacviqgvvgtetpmlkedsilavr 120
|||||
Qy 61 QQIFNLFSTKDSAAAWDETLLDKFYTELYQQLDLEACVIQGVGVTEPTLMKEDSILAVR 120

Db 121 kyfqritylylkekyspcawev-raeimrfsfstnlqeslrake 164
|||||
Qy 121 KYFQRITYLYLKEKYSPCWEEVRAEIMRFSFSLTNLQESLSRSKE 165

Search completed: Tue Aug 29 17:07:31 1995
Job time : 15 secs.


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[3]
RN SEQUENCE FROM N.A.
RP
RM 87060261
RA LAMN R.M., GROSS M., HOUCK C.M., FRANK A.E., GRAY P.V.,
RA GOEDDEL D.V.;
RL PROC. NATL. ACAD. SCI. U.S.A. 78:5435-5439(1981).
[4]
RN SEQUENCE OF 7-188 FROM N.A.
RP
RM 81015442
RA STREILI M., NAGATA S., WEISSMANN C.;
RL SCIENCE 209:1343-1347(1980).
[5]
RN SEQUENCE OF 24-112 AND 136-188.
RP
RM 81052321
RA ALLEN G., FANTES K.H.;
RL NATURE 287:408-411(1980).
[6]
RN DISULFIDE BONDS.
RP
RM 81123083
RA METZEL R.;
RL NATURE 289:606-607(1981).
[7]
RN 3D-STRUCTURE MODELLING.
RP
RM 94052087
RA MURGOLO N.J., WINDSOR W.T., HRUZA A., REICHERT P., TSARBOPOULOS A.,
RA BALDWIN S., HUANG E., PRAMANIK B., EALICK S., TROTTA P.P.;
RL PROTEINS 17:62-74(1993).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; V00548; HSIFR6.
DR EMBL; V00549; HSIFR7.
DR PIR; A01827; IVHUA2.
DR PIR; A01828; IVHUA3.
DR PDB; 2HIE; 31-AUG-94.
DR MIM; 147562; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON_ALPHA_BETA.
KW CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL; 3D-STRUCTURE.
FT SIGNAL 1 23
FT CHAIN 24 188 INTERFERON ALPHA-2.
FT DISULFID 24 121
FT DISULFID 52 161
FT CONFLICT 46 46 K -> R (IN REF. 3 AND 4).
SQ SEQUENCE 188 AA; 21550 MW; 189049 CN;

DB 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 2.34e-229;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdlpqthslgsrrtllmlagmkialfscldkdrhdfgfpqeeefgnqfkaetipvlhemi 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 CDLPQTHSLGSRRTLLMLAQMRRISLFSCLKORRDFGFPQEEFGNQFKAETIPVLHEMI 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 84 qqifnlfstkdssaaawdetllldkfyetelyqqindleacviqgvgtetpmlkedsilavr 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 QQIFNLFSTKSSAAWDETLLDKFYETELYQQINDLEACVIQGVGTETPLMKEDSILAVR 120
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 144 kyfqrtilylkekyspcawevvraeimsrfselstnlqeslsrke 188
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 KYFQRITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRSKE 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 2
ID INAS_HUMAN STANDARD; PRT; 189 AA.

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AC P01569;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 13-AUG-1987 (REL. 05, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-5 PRECURSOR (INTERFERON ALPHA-G) (LEIF G) (INTERFERON
DE ALPHA-61).
GN IFNA5.
OS HOMO SAPIENS (HUMAN).
OC EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
OC EUTHERIA; PRIMATES.
RN [1]
RP SEQUENCE FROM N.A.
RM 86037205
RA HENCO K., BROSIUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,
RA HOCHSTADT J., KOVACIC T., PASEK M., SCHAMBOECK A., SCHMID J.,
RA TODOKORO K., WAELECHLI M., NAGATA S., WEISSMANN C.;
RL J. MOL. BIOL. 185:227-260(1985).
RN [2]
RP SEQUENCE OF 57-189 FROM N.A.
RM 81148795
RA GOEDDEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAMN R.M.,
RA MCCANDLISS R., SEEBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;
RL NATURE 290:20-26(1981).
CC -1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL
CC ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.
CC -1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR EMBL; X02956; HSIFNA5.
DR EMBL; V00541; HSIFR13.
DR PIR; A01833; IVHUA7.
DR HSSP; P01563; ZHIE.
DR MIM; 147565; 11TH EDITION.
DR PROSITE; PS00252; INTERFERON_ALPHA_BETA.
KW CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT SIGNAL 1 23
FT CHAIN 24 189 INTERFERON ALPHA-5.
FT DISULFID 24 122 BY SIMILARITY.
FT DISULFID 52 162 BY SIMILARITY.
SQ SEQUENCE 189 AA; 21942 MW; 184346 CN;

DB 4; Score 1074; Match 84.9%; QryMatch 87.9%; Pred. No. 1.12e-199;
Matches 141; Conservative 15; Mismatches 9; Indels 1; Gaps 1;

Db 24 cdlpqthslgsrrtllmlagmkialfscldkdrhdfgfpqeeefgnqfkaetipvlhemi 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 CDLPQTHSLGSRRTLLMLAQMRRISLFSCLKORRDFGFPQEEFGNQFKAETIPVLHEMI 59
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 84 iqqifnlfstkdssaaawdetllldkfyetelyqqindleacviqgvgtetpmlkedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYETELYQQINDLEACVIQGVGTETPLMKEDSILAV 119
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

Db 144 rkyfqrtilylkekyspcawevvraeimsrfselstnlqeslsrke 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 RKYFQRITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRSKE 165
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 3
ID INAD_HUMAN STANDARD; PRT; 189 AA.
AC P01570;
DT 21-JUL-1986 (REL. 01, CREATED)
DT 21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT 01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE INTERFERON ALPHA-14 PRECURSOR (INTERFERON ALPHA-H) (LEIF H)
DE (INTERFERON LAMBDA-2-H).

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[illegible][illegible]

[3]		
RP	SEQUENCE FROM N.A.	
RP		
RM	81148795	
RA	GOEDEL D.V., LEUNG D.W., DULL T.J., GROSS M., LAWN R.M.,	
RA	MCCANDLESS R., SEERBURG P.H., ULLRICH A., YELVERTON E., GRAY P.W.;	
RL	NATURE 290:20-26(1981).	
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL	
CC	ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:	
CC	A PROTEIN KINASE AND AN OLIGODENYLATE SYNTHETASE.	
CC	-1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.	
CC	EMBL; X03125; HSIFNA8.	
DR	EMBL; V00550; HSIFR8.	
DR	PIR; D23753; IVHU18.	
DR	PIR; A01829; IVHU04.	
DR	HSSP; P01563; 2HIE.	
DR	MIM; I47568; 11TH EDITION.	
DR	PROSITE; P500252; INTERFERON ALPHABETA.	
KW	CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.	
FT	SIGNAL	1
FT	CHAIN	24 189
FT		INTERFERON ALPHA-8.

FT	DISULFID	24	122	BY SIMILARITY.
FT	DISULFID	52	162	BY SIMILARITY.
FT	CONFLICT	8	8	L -> M (IN REF. 2 AND 3).
FT	CONFLICT	121	124	SCVM -> VLCD (IN REF. 2 AND 3).
SQ	SEQUENCE	189 AA;	21989 MW;	187461 CN;
DB	4; Score	1012;	Match 82.5%;	OryMatch 82.8%; Pred. No. 3,40e-186;
	Matches	137;	Conservative	13; Mismatches 15; Indels 1; Gaps 1;
Db	24	cdlpqthslgnrrailagmrriispciskdrhdfefgqddkqfkaqaisvlhem	83	
Qy	1	CDLPQTHSLGSRRTIILQAQRRIISFLCKDRDRDFGFFQEEFGN-QFQAETIVLVHEM	59	
Db	84	iqqtnlfsktdsaaletdlldfyieldqqlndlescvmqevqvtesplmyedsilav	143	
Qy	60	IQQTFNLFSTKDSAAWDETLLDKFYELQQLNDLEACVIGQGVGTETPLMKEDSILAV	119	
Db	144	kyfqrtilytkkyscawewvraeimrfsislnlqtrikeke	189	
Qy	120	KYFQRIYLYKKEKYSFCAWEVVRAEIMRFSISLNIAQESLRKSE	165	

RESULT	11
ID	INA7 HUMAN STANDARD; PRT; 189 AA.
AC	P01567;
DT	21-JUL-1986 (REL. 01, CREATED)
DT	21-JUL-1986 (REL. 01, LAST SEQUENCE UPDATE)
DT	01-FEB-1995 (REL. 31, LAST ANNOTATION UPDATE)
DE	INTERFERON ALPHA-7 PRECURSOR (INTERFERON ALPHA-J1) (INTERFERON DE ALPHA-J) (LEIF J).
GN	IFNA7.
OS	HOMO SAPIENS (HUMAN).
OC	EUKARYOTA; METAZOA; CHORDATA; VERTEBRATA; TETRAPODA; MAMMALIA;
CC	EUTHERIA; PRIMATES.
RN	[1]
RP	SEQUENCE FROM N.A.
RM	86037205
RA	HENCO K., BROSIUS J., FUJISAWA A., FUJISAWA J.-I., HAYNES J.R.,
RA	HODOSTADT J., KOVACHIC T., PASEK M., SCHAMBOECK A., SCHMID J.,
RA	TOKORO K., WÄELCHLI M., NAKAGAI S., WEISSMANN C.;
RL	J. MOL. BIOL. 185:227-260(1985).
RN	[2]
RP	SEQUENCE FROM N.A.
RM	83010248
RA	ULIRICH A., GRAY A., GOEDEL D.V., DULL T.J.;
RA	J. MOL. BIOL. 156:467-486(1982).
CC	-1- FUNCTION: PRODUCED BY MACROPHAGES, IFN-ALPHA HAVE ANTIVIRAL ACTIVITIES. INTERFERON STIMULATES THE PRODUCTION OF TWO ENZYMES:
CC	A PROTEIN KINASE AND AN OLIGOADENYLATE SYNTHETASE.
CC	-1- SIMILARITY: TO ALPHA-II AND BETA-INTERFERONS.
DR	EMBL; X02960; HSFNAT7.
DR	PIR; A01831; IVHUAO.
DR	HSP; P01563; ZHF.
DR	MIM; I47567; 11TH EDITION.
DR	PROSITE; PS00252; INTERFERON ALPHABETA.
KW	CYTOKINE; ANTIVIRAL; MULTIGENE FAMILY; SIGNAL.
FT	SIGNAL 1 23
FT	CHAIN 24 189 INTERFERON ALPHA-7.
FT	DISULFID 24 122 BY SIMILARITY.
FT	DISULFID 52 162 BY SIMILARITY.
SQ	SEQUENCE 189 AA; 22106 MW; 185066 CN;
DB	4; Score 1012; Match 79.5%; QryMatch 82.8%; Pred. No. 3.40e-186;
Matches	132; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

(ML)

The diagrams show the following linkage configurations:

- (ML): A single horizontal bar with a vertical bar attached to its midpoint.
- (MM): A horizontal bar with a vertical bar attached to its left end.
- (NN): A horizontal bar with a vertical bar attached to its left end, and a diagonal bar attached to its right end.
- (OO): A horizontal bar with a vertical bar attached to its left end, and a diagonal bar attached to its right end.
- (PP): A horizontal bar with a vertical bar attached to its left end, and a diagonal bar attached to its right end.
- (QQ): A horizontal bar with a vertical bar attached to its left end, and a diagonal bar attached to its right end.

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 29 19:01:10 1995; MasPar time 54.70 Seconds
810.721 Million cell updates

Tabular output not generated.

Title: >US-08-249-671-8

Description: (1:869) from US08249671.seq

Perfect Score:

N.A. Sequence: 1 GAATTCGAGATTATCGTCAC.....TGATAACGATCGTAACGCA 869
Comp: CTTAAGCTCTAATAGCAGTG.....ACTATTGCTAGCATTTGAGGT

Scoring table: TABLE default

Gap 6

Nmatch STD : Dbase 0: Query 0

Searched: 61539 seqs. 25515148 bases x 2

Database: n-genes

```

1 n-qenl

```

2 n-gen2

3 n-gen3

4 n-gen4

n-gen5

n-gen6

h-gen / h-geng

n-gen9

10 n-gen10

11 n-gen11

Statistics: Mean 9.222; Variance 5.827; scale 1.582

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	500	57.5	639	3	Q20764		Human IFNalpha 2C gen	2.46e-310
2	500	57.5	639	3	Q20731		pAD198-IFN HindIII/Xb	2.46e-310
3	498	57.3	589	3	N50272		DNA encoding interfer	5.53e-309
4	498	57.3	501	2	N70528		Sequence encoding IFN	5.53e-309

ALIGNMENTS

RESULT	1
ID	Q20764 standard; DNA; 639 BP.
ACC	Q20764;
DEF	21-APR-1992 (first entry)
DT	Human IFNalpha 2C gene from pAD198-IFN.
DDT	Interferon; O-glycosylation; ss.
KW	Homo sapiens.
OS	Homo sapiens.
SF	Key Location/Qualifiers
FT	CDS 57..623
FT	*tag= a
FT	/label= huIFNalpha
FT	sig_peptide 57..125
FT	*tag= b
FT	mat_peptide 126..623
FT	*tag= c
FT	DEA021917-A.
PN	DEA021917-A.
PD	16-JAN-1992.
PR	10-JUL-1990; 021917.
PR	10-JUL-1990; DE-021917.

PA (BOEH) BOEHRINGER INGELHEIM.
PI Himmler A, Adolf G;
DR WPI; 92-025485/04.
DR P-PSDB; R20549.
PT O-glycosylated alpha-interferon, used as medicament - isolated
PT following secretion into conditioned medium of mammalian cells
PT contg. a suitable expression plasmid
PS Disclosure; Fig 6; 24pp; German.
CC Human embryonic kidney cells transformed with the human IFNalpha
CC 2C gene, contd. in pAD19B-IFN, are grown under suitable conditions.
CC O-glycosylated IFNalpha can then be isolated and purified from the
CC tissue culture supernatant.
CC See also Q20764-66 and Q22517-29.
SQ Sequence 639 BP; 171 A; 155 C; 152 G; 161 T;

DB 3; Score 500; Match 99.8%; QryMatch 57.5%; Pred. No. 2.46e-310;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 tgtgatctgctcaaacccacagctgggtagcaggagaccttgatgctctggcacag 185
|||||
Qy 355 TGTGATCTGCTCAAAACCACAGCCTGGGTAGCAGGAGGACTTGATGCTCTGGCACAG 414

Db 186 atgaggagaatctctcttctctctgcttgaggagacagctgaacttggattccccag 245
|||||
Qy 415 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGACTTTGGATTTCCCGAG 474

Db 246 gaggagtttgcaaacagcttccaaaggctgaaacccatccctgtctccatgatgatgc 305
|||||
Qy 475 GAGGAGTTTGGCAACGATCTCCAAAGGCTGAAACCATCCCTGTCTCCATGAGATGATC 534

Db 306 cagcagatcttcaatctctcagcaaaaggactcatctgctgttgggatgagaccctc 365
|||||
Qy 535 CAGCAGATCTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGGATGAGACCTC 594

Db 366 ctagacaaattctacactgaactctaccagcagctgaatgaactcgaactctgtgata 425
|||||
Qy 595 CTAGACAAATCTTACACTGAACTCTACAGCAGCTGATGACCTGGAAGCCTTGTGATA 654

Db 426 aaatcttccaaagaatcactctctatctgaaagagaagaatacacagccttggctgg 545
|||||
Qy 715 AAATACTTCCAAAGAAATCACTCTATCTGAAAGAGAAATATACAGCCCTTGTGCTGG 774

Db 546 gagggtgtcagacgaataatcatgagatcttttcttcttccaaacatgcagaagaat 605
|||||
Qy 775 GAGGTTGTGAGAGCAGAAATCATGAGATCTTTTCTTTGTCAAACAAATTCGAAGAAAT 834

RESULT 2
ID Q20731 standard; DNA; 639 BP.
AC Q20731;
DT 19-MAY-1992 (first entry)
DE pAD19B-IFN HindIII/XbaI insert.
KW Interferon; IF7; beta-globulin; ss.
FH Key Location/Qualifiers
FT CDS 9..623
FT /*tag= a

FT /label= IFN-alpha2c
PN W09201055-A.
PD 23-JAN-1992.
PF 06-JUL-1991; E01266.
PR 10-JUL-1990; DE-021917.
PR 12-NOV-1990; DE-035877.
PA (BOEH) BOEHRINGER INGELHEIM.
PI Adolf G, Himmler A, Ahorn HU, Kalsner I, Maurer-Fogy I;
DR WPI; 92-056870/07.
DR P-PSDB; R20564.
DR O-glycosylated alpha-interferon - used for treatment of
PT viral of tumour diseases
PS Disclosure; Fig 6(A+B); 104pp; English.
CC Plasmid pAD-CMV19 (6.1 kb) is incubated with HindIII and XbaI, then
CC ligated with a modified cDNA fragment for human IFN-alpha2c. This
CC fragment is obtd. from the known clone IF7 by PCR-modification of
CC the 5'-noncoding region to replace it with the corresp. region from
CC human beta-globulin mRNA. This modification significantly improves
CC expression by increasing the efficiency of initiation of translation.
CC The recombinant prod. is designated pAD19B-IFN.
CC See also Q20731-43 and Q20522-26.
SQ Sequence 639 BP; 171 A; 155 C; 152 G; 161 T;

DB 3; Score 500; Match 99.8%; QryMatch 57.5%; Pred. No. 2.46e-310;
Matches 501; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 126 tgtgatctgctcaaacccacagctgggtagcaggagaccttgatgctctggcacag 185
|||||
Qy 355 TGTGATCTGCTCAAAACCACAGCCTGGGTAGCAGGAGGACTTGATGCTCTGGCACAG 414

Db 186 atgaggagaatctctcttctctctgcttgaggagacagctgaacttggattccccag 245
|||||
Qy 415 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGACTTTGGATTTCCCGAG 474

Db 246 gaggagtttgcaaacagcttccaaaggctgaaacccatccctgtctccatgatgatgc 305
|||||
Qy 475 GAGGAGTTTGGCAACGATCTCCAAAGGCTGAAACCATCCCTGTCTCCATGAGATGATC 534

Db 306 cagcagatcttcaatctctcagcaaaaggactcatctgctgttgggatgagaccctc 365
|||||
Qy 535 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGGATGAGACCTC 594

Db 366 ctagacaaattctacactgaactctaccagcagctgaatgaactcgaactctgtgata 425
|||||
Qy 595 CTAGACAAATCTTACACTGAACTCTACAGCAGCTGATGACCTGGAAGCCTTGTGATA 654

Db 426 cagggggtgggggtgacagagactcccctgatgaggaggactccattctgtgctgag 485
|||||
Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCCCTGATGAGAGGAGACTCCCATTTCTGGCTGAGG 714

Db 486 aaatcttccaaagaatcactctctatctgaaagagaagaatacacagccttggctgg 545
|||||
Qy 715 AAATACTTCCAAAGAAATCACTCTATCTGAAAGAGAAATATACAGCCCTTGTGCTGG 774

Db 546 gagggtgtcagacgaataatcatgagatcttttcttcttccaaacatgcagaagaat 605
|||||
Qy 775 GAGGTTGTGAGAGCAGAAATCATGAGATCTTTTCTTTGTCAAACAAATTCGAAGAAAT 834

Db 606 ttaagaagtaaggaatgaaac 627
|||||
Qy 835 TTAAGAGTAAGGAATGATAAC 856

RESULT 3

ID N50272 standard; DNA; 589 BP.
AC N50272;
DE 24-NOV-1991 (first entry)
DT DNA encoding interferon alpha-2 .
KW Interferon alpha-2; ss DNA; hybrid DNA sequence; crossover region.
FH Key Location/Qualifiers
FT CDS 1..498
FT /*tag= a
FT misc feature 184..194
FT /*tag= b
FT /note= "crossover region A"
FT misc feature 258..282
FT /*tag= c
FT /note= "crossover region B"
FT misc feature 258..299
FT /*tag= d
FT /note= "crossover region C"
FT misc feature 258..315
FT /*tag= e
FT /note= "crossover region D"
FT misc feature 322..336
FT /*tag= f
FT /note= "crossover region E"
FT misc feature 338..348
FT /*tag= g
FT /note= "crossover region F"
FT misc feature 372..391
FT /*tag= h
FT /note= "crossover region G"
FT misc feature 393..450
FT /*tag= i
FT /note= "crossover region H"
FT misc feature 453..458
FT /*tag= j
FT /note= "crossover region I"
FT misc feature 459..479
FT /*tag= k
FT /note= "crossover region J"
FT misc feature 514..519
FT /*tag= l
FT /note= "crossover region K"
PN EP-141484-A.
PD 15-MAY-1985.
PF 05-JUN-1984; 303787.
PR 10-JUN-1983; GB-015980.
PA (BIOJ) Biogen NV.
PI Weissmann C, Weber H.
WPI; 85-117654/20.
DR P-PSDB; P50228.
PT New hybrid DNA sequences and hybrid polypeptide(s) - useful in prodn.
PT of interferon(s), lymphokines, viral antigens, etc.
PS Disclosure; Fig. 6A-C; 47pp; English.
CC The DNA encodes interferon alpha-2. The DNA may be fused to a second coding sequence, eg for animal or human alpha, beta or gamma-interferons, lymphokines, foot-and-mouth disease antigens, to form a hybrid DNA. The DNA must be fused to the second DNA sequence in the same reading frame to maintain a constant reading frame through a crossover region common to both sequences. The hybrid sequences are obtd. without the need for chance availability of restriction sites to be combined. Sequential deletions to give prods. with modified properties, activity and specificity are reliable.
SQ Sequence 589 BP; 165 A; 135 C; 135 G; 154 T;
DB 3; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 5.53e-309;

Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 tqgatctgcctcaaacacacagcctgggtagcagagagagccttgatgctcctggcacag 60
|||||
Qy 355 TGTGATCTGCCCTCAAAACCCACAGCGCTGGGTAGCAGGAGGACCTTGATGCTCGGCACAG 414
|||||
Db 61 atgaggagaatctctcttctcctgcttgaggagacagacatgactttggatttccccag 120
|||||
Qy 415 ATGAGGAGAATCTCTCTTTCTCTGCTTTGAAGGACAGACGCTGACTTTGGATTTCGCCAG 474
|||||
Db 121 gaggagttagcaaccagttccaaaaggctgaaccatccctgtcctccatgagatgac 180
|||||
Qy 475 GAGGAGTTTGGCAACCCAGTCCAAAAGGCTGAACCATCCCTGTCTCCATCAGATGATC 534
|||||
Db 181 cagcagatcttcaatctcttcagcaacaaggactcatctgctgttgaggatgagacocctc 240
|||||
Qy 535 CAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTTGGGATCAGACCCCTC 594
|||||
Db 241 ctagaacaattctacactgaactctaccagcagctgaatgacctgaagcctgtgtgata 300
|||||
Qy 595 CTAGACAAATTTACACTGAACTCTACCAGCAGCTGAATGACCTGGAGCCCTGTCTGATA 654
|||||
Db 301 cagggggtgggggtgacagagactccctgatgaaggagagactccattcctggctgtgagg 360
|||||
Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATGAAGGAGACTCCATTTCTGCTGTCAGG 714
|||||
Db 361 aaatacttccaaagaatcactctctatctgaaagagaagaatacacagcccttgctgtg 420
|||||
Qy 715 AATATCTTCCAAAGATCAGCTCTCTATCTGAAAGACAGAAATACAGCCCTTGTGCTGG 774
|||||
Db 421 gaggtgtcagcagcagaatcatgagatcttttttctgtcaacaacttgaagaagt 480
|||||
Qy 775 GAGGTGTGACAGCAGAAATCATGAGATCTTTTCTTGTCAACAACTTGAAGAAAGT 834
|||||
Db 481 ttaagaagtgaaggaatgaaac 502
|||||
Qy 835 TTAAAGTAAGGAATGATAAC 856
|||||
RESULT 4
ID N70528 standard; DNA; 501 BP.
AC N70528;
DT 20-MAY-1991 (first entry)
DE Sequence encoding IFN-alpha-2 (Arg).
KW Hybrid alpha/omega interferon; antiviral; virucide; antitumour;
KW cytostatic; ss.
FH Key Location/Qualifiers
FT CDS 1..501
FT /*tag= a
PN EP-236920-A.
PD 16-SEP-1987.
PF 04-MAR-1987; 103030.
PR 10-MAR-1986; DE-607835.
PA (BOEH) BOEHRINGER INGELHEIM.
PI Hauptmann R, Swetly P, Meindl P, Gunther A, Falkner E,
PI Bodo G, Maurer-Fogy I;
DR WPI; 87-258223/37.
DR P-PSDB; P70329.
PT New hybrid interferon prods. useful as antiviral agents - contg.
PT alpha and omega interferon fragments
PS Disclosure; pp4-6; 65pp; German.
CC Hybrid interferons comprising a fragment of an alpha-interferon and
CC a fragment of an omega-interferon, and their N-terminal Met or
CC N-formyl-Met derivs. and N-glycosylated derivs., are new. The hybrid

CC interferons are useful as antiviral and antitumour agents. Both IFN-
 CC alpha-2(Arg) and omega-1-interferon has a 191-196 BglII restriction
 CC site (see N70528 and N70529). In addition, IFN-alpha-2(Arg) has a
 CC 451-456 BglIII site.
 SQ Sequence 501 BP; 141 A; 116 C; 123 G; 121 T;

DB 2; Score 498; Match 100.0%; QryMatch 57.3%; Pred. No. 5.53e-309;
 Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 tttgatctgctcaaacacacagctgggtagcagagagacattgatctctggcacag 63
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 355 TGTGATCTGCTCAAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCTCGGCACAG 414

Db 64 atgagagaatctcttcttctctgcttggaagacagcgtgacttggattccccag 123
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 415 ATGAGAGAAATCTCTCTTCTCTCTTGAAGCAGACAGCTGACTTTGGATTTCCCCAG 474

Db 124 gaggagtttgcaaccagttccaaaaggctgaaccatccctgtctccatgagatgac 183
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 475 GAGGAGTTTGGCAACACAGTTCBAAGGCTGMAACCATCCCTGTCTCCATGAGATGATC 534

Db 184 cagcagatctcaatctctcagcaaaagagctcatctgctgtggatgagaccctc 243
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGAGCACTATCTGCTGGGATGAGACCCCTC 594

Db 244 ctagacaaattctacatgaactctaccagcagcgaatgaactggaagcctgtgtgata 303
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 595 CTAGACAAATTTACACTGAACCTTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654

Db 304 caggggtgggggtgacagagactccctgatgaagagagactccattctggctgtgag 363
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 655 CAGGGGTGGGGGTGACAGACACTCCCTGATGAAGGAGACTCCATTTCTGGCTGTGAGG 714

Db 364 aaattactccaagaatcaactctctatctgaaagagaagaatacacgacctgtgctgg 423
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 715 AAATACTTCCAAAGAATCACTCTCTATCTGAAGAAGAAATACAGCCCTTGTGCTGG 774

Db 424 gaggtgtcagagcaagaatcatgagatcttttcttctgaacaacttgcagaagaat 483
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 775 GAGGTGTGACAGCAAAATCATGATCTTTTCTTTTCTCAACAACCTTCCAGAAAGT 834

Db 484 ttaagaagtaagaatga 501
 ||||||||||||||||
 Qy 835 TTAAGAGTAAGCAATGA 852

RESULT 5
 ID N60399 standard; DNA; 1863 BP.
 AC N60399;
 DT 25-JUN-1991 (first entry)
 DE Sequence of the promoter region 22 of the alca gene, the synthetic
 DE signal peptide coding region 68 and the coding region 60 coding for
 DE human interferon alpha-2 in pALCAL5IFN.
 KW Filamentous fungi promoter; ds.

FH Key Location/Qualifiers
 FT misc feature 29
 FT /*tag= a
 FT /*note= * = base 1200*
 FT sig_peptide 878..922
 FT /*tag= b
 FT CDS 923..975
 FT /*tag= c
 FT mat_peptide 976..1474
 FT /*tag= d

PN W08606097-A.
 PD 23-OCT-1986.
 PF 14-APR-1986; G00209.
 PR 15-APR-1985; CA-479135.
 PR 20-DEC-1985; US-811404.
 PA (ALIE-) ALLELIX INC.
 PI Gwynne DI, Buxton F, Pickett M, Davies R, Scazzocchio C;
 DR WPI; 86-291664/44.
 PT DNA construct for use in filamentous fungi - comprising promoter
 PT operative in filamentous fungi to promote transcription of coding
 PT region
 PS Disclosure; Fig 11; 75pp; English.

CC In the constructs of the invention, the promoter region naturally
 CC associated with the alcohol dehydrogenase I (alcaA) gene and the
 CC aldehyde dehydrogenase (aldA) gene of *A. nidulans* or naturally
 CC associated with the glucoamylase gene in *Aspergillus niger* may be
 CC used. The DNA construct may contain a promoter region in operative
 CC association with a signal peptide coding region. The promoter/signal
 CC construct is suitably provided with a flanking restriction site to
 CC allow precise coupling of the protein coding region to the signal
 CC peptide coding region.

SQ Sequence 1863 BP; 516 A; 425 C; 422 G; 500 T;
 DB 2; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 5.53e-309;
 Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 977 tbtgatctgctcaaacacacagctgggtagcagagagacattgatctctggcacag 1036
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 355 TGTGATCTGCTCAAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCTCGGCACAG 414

Db 1037 atgagagaatctcttcttctctgcttggaagacagacatgacttttgattccccag 1096
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 415 ATGAGAGAAATCTCTCTTCTCTCTTGAAGCAGACAGCTGACTTTGGATTTCCCCAG 474

Db 1097 gaggagtttgcaaccagttccaaaaggctgaaccatccctgtctccatgagatgac 1156
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 475 GAGGAGTTTGGCAACACAGTTCBAAGGCTGMAACCATCCCTGTCTCGCATGATGATC 534

Db 1157 cagcagatctcaatctctcagcaaaagagactcatctgctgtggatgagaccctc 1216
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 535 CAGCAGATCTTCAATCTCTTACAGCAAAAGAGCACTATCTGCTTGGATGACACCCCTC 594

Db 1217 ctagacaaattctacatgaactctaccagcagcgaatgaactggaagcctgtgtgata 1276
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 595 CTAGACAAATTTACACTGAACCTTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654

Db 1277 caggggtgggggtgacagagactccctgatgaagagagactccattctggctgtgag 1336
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 655 CAGGGGTGGGGGTGACAGACACTCCCTGATGAAGAGAGACTCCATTTCTGGCTGTGAGG 714

Db 1337 aaattactccaagaatcaactctctatctgaagagaagaatacacgacctgtgctgg 1396
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 715 AAATACTTCCAAAGAATCACTCTCTATCTGAAGAAGAAATACAGCCCTTGTGCTGG 774

Db 1397 gaggtgtcagagcagaagaatcatgagatcttttcttctgaacaacttgcagaagaat 1456
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 775 GAGGTGTGACAGCAAAATCATGATCTTTTCTTTTCTCAACAACCTTCAAGAAGT 834

Db 1457 ttaagaagtaagaatgaaac 1478
 ||||||||||||||||
 Qy 835 TTAAGAGTAAGCAATGATAC 856

RESULT 6

ID N10011 standard; DNA; 744 BP.
AC N10011;
DT 13-AUG-1992 (first entry)
DE Sequence of the Hif-II-206 fragment of culture HcIF-G encoding
KW Interferon (IFN) -alpha-2 and signal sequence.
DE Anti-viral agent; anti-cancer agent; therapy; tumour; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 2..52
FT /*tag= a
FT mat_peptide 53..550
FT /*tag= b
PN EP--32134-A.
PD 15-JUL-1981.
PF 07-JAN-1981; 300050.
PR 08-JAN-1980; EP-300079.
PR 03-APR-1980; EP-301100.
PR 02-OCT-1980; GB-031737.
PA (BIOJ) BIOGEN NV.
PI Weisemann G;
DR WPI; 81-53697D/30.
DR P-PSDB; P10018.
PT DNA sequences coding for interferon-like polypeptide(s) - useful
PT as antiviral or antitumour agents
PS Claim 6; Fig 12-16; 136pp; English.
CC The inventors claim DNA sequences coding for interferon-like
CC polypeptide(s). The DNA sequences pref. encode IFN-alpha type 1, 2,
CC 4a and 4b. Pref. DNA sequences which hybridise to the inserts of 2-
CC pBR322(pst)/HcIF-4c, 2-pBR322(pst)/HcIF-2h, 2-pBR322(pst)/HcIF-SN35,
CC 2-pBR322(pst)/HcIF-SN42 and 2-pBR322(pst)/HcIF-2h-AH6 comprise
CC 2-pBR322(pst)/HcIF-II-206, 2-pBR322(pst)/HcIF-SN35-AHL6, and
CC Hif-chrl, -3, -12, -13, -16-1, -26, -30, -35, -19 and -27. Pref.
CC recombinant DNA molecules are C8-IFN-alpha-1, C8-IFN-alpha-2,
CC LAC-AUG(alpha-2) and beta-lac-AUG(alpha-2). A comparison of the
CC nucleotide sequence of the coding region of HcIF-35HB-alpha and
CC that of Hif-2h (coding region) reveals that they are identical.
SQ Sequence 744 BP; 202 A; 171 C; 169 G; 202 T;

DB 4; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 5.53e-309;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 53 tttgatctgctcaaacccacagcctgggttagcaggagaccttgatctctcggcacag 112
|||||
Qy 355 TGTGATCTGCTCAAAACCCACAGCCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414
|||||
Db 113 atgaggagaatctctcttctctgctgctgaaagacagacatgactttggattcccccag 172
|||||
Qy 415 ATGAGAGAAATCTCTCTTTCTCTGCTTGAAGAGCAGACGCTGACTTTGGATTTCCCCAG 474
|||||
Db 173 gaggagtttgcaacacagtttccaaagcgtgaacacatccctctctccatgagatgac 232
|||||
Qy 475 GAGGAGTTTGGCAACAGTCTCCAAAAGGCTCAAAACATCCCTGCTCCATGAGATGATC 534
|||||
Db 233 cagcagatctcaatctcttcacgacaaaggactcatctgctgtggatgagaccctc 292
|||||
Qy 535 CAGCAGATCTTCAATCTCTTTCACGAAAGGACTATCTGCTGCTTGGGATGAGACCTC 594
|||||
Db 293 ctagacaaattctcaactgaactctaccagagctgaatgacctggaagcctgtgtgata 352
|||||
Qy 595 CTAGACAAATTTCACTGAACTCTACACGACCTGAATGACCTGGAGCCCTGTGTGATA 654
|||||
Db 353 caggggggtgggggtgacagagactccctgatgaaaggagactccattctgctgtgag 412
|||||
Qy 655 CAGGGGGTGGGGGTGACAGAGACTCCCTGATGAGGAGGAGCTCCATTTCTGGCTGTGAGG 714
|||||

Db 413 aaatacttccaagaatcactctctatctgtgaagaagaagaatacagcccttgctgctgg 472
|||||
Qy 715 AAATACTTCCAAAGAACTACTCTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGG 774
|||||
Db 473 gagggtgtcagagcagaatacatgagatcttttcttcttcaacaaacttgcaagaagt 532
|||||
Qy 775 GAGGTGTGTCAGAGAGAAATCATGAGATCTTTTCTTGTCAACAACAACTTGCAGAAAGT 834
|||||
Db 533 ttaagaagtaaggaatgaaac 554
|||||
Qy 835 TTAGCAAGTAAGGAATGATAAC 856
|||||

RESULT 7
ID N20090 standard; cDNA; 958 BP.
AC N20090;
DT 10-AUG-1992 (first entry)
DE Sequence of leukocyte interferon Leif A cDNA.
KW Viral infection; therapy; malignancy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 60..626
FT /*tag= a
PN GB2079291-A.
PD 20-JAN-1982.
PF 01-JUL-1981; 120279.
PR 01-JUL-1980; US-164986.
PR 08-SEP-1980; US-184909.
PR 10-NOV-1980; US-205578.
PR 21-APR-1981; US-256204.
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (GENE-) GENENTECH INC.
PI Goeddel DYN, Pestka S;
DR WPI; 82-04460E/03.
DR P-PSDB; P20103.
PT Mature human leukocyte interferon polypeptide(s) - prepd. from
PT microbes transformed with appropriate DNA sequences
PS Claim 34; Fig 3; 20pp; English.
CC The inventors claim a polypeptide comprising the AA sequence of a
CC mature human Leif and a DNA sequence encoding it. Leif A-D, F, H-J
CC and encoding DNA are specifically claimed. They are natural allelic
CC variations. Leif is isolated from the leukocytes of humans with
CC chronic myelogenous leukaemia, induced to produce interferon with
CC Sendai or Newcastle disease virus; esp. the cell line KG-1.
SQ Sequence 958 BP; 266 A; 211 C; 193 G; 288 T;

DB 4; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 1.24e-307;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 tttgatctgctcaaacccacagcctgggttagcaggagaccttgatctcctggcacag 189
|||||
Qy 355 TGTGATCTGCTCAAAACCCACAGCCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414
|||||
Db 190 atgaggaataatctcttctctctctgctgaaagacagacatgactttggattcccccag 249
|||||
Qy 415 ATGAGGAGAAATCTCTCTTTCTCTGCTTCAAGCAGACGCTGACTTTGGATTTCCCCAG 474
|||||
Db 250 gaggagtttggcaaccaggttccaaaggctgaaacatccctgtctccatgagatgac 309
|||||
Qy 475 GAGGAGTTTGGCAACCACTTCCAAAGGCTGAAACCCTCCCTGCTCTCCATGAGATGATC 534
|||||
Db 310 cagcagatcttcaatctcttcagcacaaggactcatctgctgcttgggagagaccctc 369
|||||

QY 535 CACGAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTTGGGATGAGACCCCTC 594
 Db 370 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
 QY 595 CTAGACAAATCTTACACTGAACCTCTACACAGCAGCTGAATGACCTGGAGCCTGTGTGATA 654
 Db 430 caggggggtgggggtgacagagactccctgatgaagagagactccattcttgctgtgaag 489
 QY 655 CAGGGGGTGGGGGTGACAGAGACTCCCTCATGATGAGGAGGACTCCATTGCTGGCTGTGAGG 714
 Db 490 aaatactccaaagaatcaactctctatctgaagagagaagaatacagccctgtgctgg 549
 QY 715 AATATCTTCCAAAGATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTGTGCTGG 774
 Db 550 gaggtgtcagagcagagaatcatgatctctttttttgtcaacaactgtcaagaagt 609
 QY 775 GAGGTGTGACAGCGAATCATGAGATCTTTTCTTTGTGTCMAAACTTCAGAAAGT 834
 Db 610 ttaagaagtaaggaatgaaac 631
 QY 835 TTAAGAGTAAGGAATGATAAC 856

RESULT 8

ID Q47153 standard; cDNA; 647 BP.
 AC Q47153;
 DT 21-JAN-1994 (first entry)
 DE Natural human interferon-alpha cDNA.
 KW IFN-alpha; hIFN-alpha; ss.
 OS Homo sapiens.
 FH Key Location/Qualifiers
 FT CDS 1..504
 FT /*tag= a
 PN EP-553494-A.
 PD 04-AUG-1993.
 PF 29-DEC-1992; 122084.
 PR 31-DEC-1991; KR-025878.
 PR 31-DEC-1991; KR-025879.
 PR 28-JAN-1992; KR-001155.
 PA (LUCK-) LUCKY LTD.
 PI Bae TO, Chang HJ, Cho JM, Park SJ, Park YM.
 DR WPI; 93-244548/31.
 DR P-PSDB; R38793.
 PT Recombinant human alpha interferon and corresp. gene - for
 PT efficient expression in yeast, and purificn. process
 PS Disclosure; Fig 1B; 30pp; English.
 CC The sequence is that of natural human interferon-alpha cDNA.
 SQ Sequence 647 BP; 174 A; 154 C; 151 G; 168 T;

DB 7; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 1.24e-307;
 Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 76 tgtatctgctcaaccacagctggtagcagagagacttgatgctctggcacag 135
 QY 355 TGTGATCTGCCCTCAACCCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCTGGGCACAG 414
 Db 136 atgagaaaatctctctttctcctgctgaagacagacatgactttgattccacag 195
 QY 415 ATGAGGAAATCTCTCTTTCTCTCTCTTGAAGGACAGACGTGACTTTGATTTCCCCAG 474
 Db 196 gaggagtgtggcaaccaggttccaaaggctgaaccatccctgtcctccatgagatgac 255
 QY 475 GAGGAGTTTGGCAACCACTTCCAAAAGGCTGAAACCATCCCTGCTCTCATGAGATGATC 534

Db 256 cagcagatcttcaatctctctcagcaacaagagactcaatctgctgttgggatgagaccctc 315
 QY 535 CACGAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTTGGGATGAGACCCCTC 594
 Db 316 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 375
 QY 595 CTAGACAAATCTTACACTGAACCTCTACACAGCAGCTGAATGACCTGGAGCCTGTGTGATA 654
 Db 376 caggggggtgggggtgacagagactccctgatgaagagagactccattcttgctgtgag 435
 QY 655 CAGGGGGTGGGGGTGACAGAGACTCCCTCATGATGAGGAGGACTCCATTGCTGGCTGTGAGG 714
 Db 436 aaatactccaaagaatcaactctctatctgaagagagaagaatacagccctgtgctgg 495
 QY 715 AATATCTTCCAAAGATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTGTGCTGG 774
 Db 496 gaggtgtcagagcagagaatcatgatgagatctttttttgtcaacaactgtcaagaagt 555
 QY 775 GAGGTGTGACAGCAGAAATCATGAGATCTTTTCTTTGTGTCMAAACTTCAGAAAGT 834
 Db 556 ttaagaagtaaggaatgaaac 577
 QY 835 TTAAGAGTAAGGAATGATAAC 856

RESULT 9

ID N30062 standard; DNA; 941 BP.
 AC N30062;
 DT 14-JUN-1992 (first entry)
 DE Sequence of a modified BamHI human interferon-alpha gene fragment.
 KW Yeast expression vector; Saccharomyces cerevisiae; promoter;
 KW glycolytic enzyme; phosphoglycerate kinase; ss.
 OS Homo sapiens.

FH Key Location/Qualifiers

FT CDS 7..534
 FT /*tag= a
 PN EP--73635-A.
 PD 09-MAR-1983.
 PF 17-AUG-1982; 408826.
 PR 25-AUG-1981; GB-025934.
 PR 23-MAR-1982; GB-008422.
 PR 16-JUN-1982; GB-017496.
 PA (KING/) KINGSMAN A J.
 PA (CELL-) CELLTECH LTD.
 PI Kingsman S M; Kingsman A J.
 DR WPI; 83-25586K/11.
 DR P-PSDB; P30163.
 PT Yeast expression vector for transforming yeasts - useful in
 PT economic prodn. of polypeptide(s) esp. human interferon-alpha
 PS Example; Fig 16; 45pp; English.
 CC The inventors claim a yeast expression vector comprising a yeast
 CC selective marker, a yeast replication origin and a yeast promoter
 CC positioned relative to a unique restriction site. The yeast
 CC promoter pref. comprises at least part of the 5' region of a gene
 CC coding for glycolytic enzyme, esp. of the yeast PGK gene located up-
 CC stream of the unique restriction site and at least part of the 3'
 CC region of the PGK gene located downstream of the site. The vector
 CC is used to express a polypeptide, eg. human interferon-alpha.
 SQ Sequence 941 BP; 315 A; 184 C; 179 G; 263 T;

DB 3; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 1.24e-307;
 Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Db 37 tgtatctgctcaaccacagctggtagcagagagacttgatgctctggcacag 96

QY 355 TGTGATCTGCCTCAAAACCCAGCCCTGGCTAGCAGGAGGACCTTGATGCTCTCGGCACAG 414
Db 97 atgagaaatctctcttctctctctgcttgaagacagacatgaatttgatttccccag 156
QY 415 ATGAGGAGAAATCTCTCTTTCTCTCTCTGCTTGAAGGACAGACGCTGCTTTGGATTTCCCCAG 474
Db 157 gaggagtttgcaaacaggttccaaagagctgaaccatccctgtctccatgatgatgc 216
QY 475 GAGGAGTTTGGCAACCAAGTTCMAAGGCTGAACCATCCCTGTCTCCATGAGATGATC 534
Db 217 cagcagatcttcaatctcttcaagcacaagagactcatctgctgcttggatgagaccctc 276
QY 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTCTTGGGATGAGACCCCTC 594
Db 277 ctagacaaattctacatgaactctaccagcagctgaatgaactggaagcctgtgtgata 336
QY 595 CTAGACAAATCTTACACTGAATCTTACGACGAGCTCAATGACCTGCAAGCCTGTGTGATA 654
Db 337 caggggttggggtgacagagactccctgatgaaggaggaactccattctgctgtgagg 396
QY 655 CAGGGGTTGGGGTGCAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGG 714
Db 397 aaatacttccaagaatcaactctctatctgaagagagaatacacagccttgtgctgg 456
QY 715 AAATACTTCCAAAGAAATCATCTATCTGAAAGAGAGAAATACAGCCCTTTGCTGG 774
Db 457 gagggttcagagcaaaatcatgagactcttttctgtcaacaaactgcaagaagt 516
QY 775 GAGGTTCAGAGCAAAATCATGATCTTTCTTCTTCAACAAACTTCGAAGAAAGT 834
Db 517 ttaagaagtaaggaatgaaac 538
QY 835 TTAAGAGTAAGGAATGATAAC 856

RESULT 10

ID Q11141 standard; DNA; 540 BP.
AC Q11141;
DT 03-JUN-1991 (first entry)
DE Interferon alpha as CR2 ligand.
KW Cellular receptor 2; CR2; binding site; BS; auto-immune disease;
KW Epstein-Barr Virus; EBV; B lymphocyte; ligand; interferon alpha; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 58..507
FT /*tag= a
FT /product= interferon alpha
FT misc RNA 274..303
FT /*tag= b
FT /*label= BS
FT /note= *fragment pref. included*
FT misc RNA 283..315
FT /*tag= c
FT /*label= BS
FT /note= *fragment most pref. included*
PN W09103251-A.
PD 21-MAR-1991.
PF 04-SEP-1990; U05027.
PR 08-SEP-1989; US-404679.
PR 20-APR-1990; US-512118.
PA (CALB-) CALIF INST BIOLOGIC.
PI Lernhardt W;
DR WPI; 91-101864/14..

DR P-PSDB; R11355.
PT DNA segment encoding CR-2 ligand and CR2 binding site - used to
PT treat auto-immune disease, B-cell lymphoma and inhibit
PT Epstein-Barr virus infection
PS Disclosure; Fig 2; 129pp; English.
CC The production of CR2 ligands including a binding site (BS) is
CC possible by transforming a cellular host with a recombinant DNA
CC mol. contg. this sequence. The ligand pref. includes a fragment
CC encoded by a sequence indicated in the features.
CC The ligand pref. contains only a single BS and has an
CC amino acid sequence <100 (pref. <20) residues in length.
CC The ligand may also comprise a plurality of the indicated segment
CC (tag c).
CC A therapeutic compsn. contg. the polypeptide is used to stimulate
CC or inhibit B lymphocyte proliferation in patients with B cell
CC lymphoma. B lymphocytes and myeloma's can be stimulated in
CC patients with immunodeficiencies and immunoglobulin secretion by
CC hybridoma cultures can be boosted.
CC The compsn. can be administered to inhibit infection in vitro or in
CC vivo by Epstein-Barr Virus.
CC See also Q11140-42.
SQ Sequence 540 BP; 153 A; 123 C; 132 G; 132 T;
DB 2; Score 492; Match 99.0%; QryMatch 56.6%; Pred. No. 6.23e-305;
Matches 497; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 13 tdtgatctgctcaaacccacagcctggtagcaggaggaccttgatgctctggcacag 72
QY 355 TGTGATCTGCCTCAAAACCCAGCCCTGGCTAGCAGGAGGACCTTGATGCTCTCGGCACAG 414
Db 73 atgagaaatctctcttctctctgcttgaagacagacatgaacttggatttccccag 132
QY 415 ATGAGGAGAAATCTCTCTTTCTCTCTGCTTGAAGGACAGACTGACTTTGGATTTCCCCAG 474
Db 133 gaggagtttgcaaacaggttccaaagagctgaacagcctctctccatgagatgac 192
QY 475 GAGGAGTTTGGCAACCACTTCCAAAAGGCTGAACCATCTCTCTCCATGAGATGATC 534
Db 193 cagcagatcttcaatctcttcagcacaagagactcatctgcttggatgagaccctc 252
QY 535 CAGCAGATCTTCAATCTCTTACGACCAAGGACTCATCTGCTCTTGGGATGAGACCCCTC 594
Db 253 ctagacaaattctacatgaactctaccagcagctgaatgacctggaagcctgtgtgata 312
QY 595 CTAGACAAATTTACACTGAACTTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654
Db 313 caggggttgagggtgacagagactccctgatgaaggaggactccattctgctgtgagg 372
QY 655 CAGGGGTTGGGGTGCAGAGACTCCCTGATCAAGGAGGACTCCATCTCTGCTGTGAGG 714
Db 373 aaatacttccaagaatcaactctctatctgaagagagaatacacagccttctgcttgg 432
QY 715 AAATACTTCCAAAGAAATCATCTCTATCTGAAGAGAGAAATACAGCCCTTTGCTGTGG 774
Db 433 gagggtggcagagcagaatcatgatgactttttcttcttcaacaaactgcaagaagt 492
QY 775 GAGGTTCAGAGCAGAGAAATCATGATGATCTTTTCTTGTTCACAAACTTCGAAGAAAGT 834
Db 493 ttaagaagtaaggaatgaaac 514
QY 835 TTAAGAGTAAGGAATGATAAC 856

RESULT 11

ID Q11142 standard; DNA; 720 BP.
AC Q11142;
DT 03-JUN-1991 (first entry)
DE Alkaline phosphatase-IFN alpha fusion as CR2 ligand.
KW Cellular receptor 2; CR2; binding site; BS; auto-immune disease;
KW Epstein-Barr Virus; EBV; B lymphocyte; IFN alpha; interferon;
KW fusion protein; ligand; ss.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 47..703
FT /tag= a
FT /product= alkaline phosphatase-IFN alpha fusion
FT protein
FT misc RNA 1..253
FT /tag= b
FT /label= alkaline phosphatase sequence
FT misc RNA 254..720
FT /tag= c
FT /label= IFN alpha sequence
FT misc RNA 470..511
FT /tag= d
FT /note= *fragment pref. included*
FT misc RNA 479..499
FT /tag= e
FT /note= *fragment most pref. included*
PN W09103251-A.
PD 21-MAR-1991.
PF 04-SEP-1990; U05027.
PR 08-SEP-1989; US-404679.
PR 20-APR-1990; US-512118.
PA (CALB-) CALIF INST BIOLOGIC.
PI Lernhardt W;
DR WPI; 91-101864/14.
DR P-PSDB; R11356.
PT DNA segment encoding CR-2 ligand and CR2 binding site - used to
PT treat auto-immune disease, B-cell lymphoma and inhibit
PT Epstein-Barr virus infection
PS Disclosure; Fig 3; 129pp; English.
CC The production of CR2 ligands including a binding site (BS) is
CC possible by transforming a cellular host with a recombinant DNA
CC mol. contg. this sequence. The ligand pref. includes a fragment
CC encoded by the total CDS and the fragment of tag e. The ligand pref.
CC contains only a single BS and has an amino acid sequence <100
CC (pref. <20) residues in length.
CC A therapeutic compsn. contg. the polypeptide is used to stimulate
CC or inhibit B lymphocyte proliferation in patients with B cell
CC lymphoma. B lymphocytes and myeloma's can be stimulated in
CC patients with immunodeficiencies and immunoglobulin secretion by
CC hybridoma cultures can be boosted.
CC The compsn. can be administered to inhibit infection in vitro or in
CC vivo by Epstein-Barr Virus.
CC See also Q11140-42.
SQ Sequence 720 BP; 176 A; 190 C; 182 G; 172 T;
DB 2; Score 492; Match 99.0%; OryMatch 56.6%; Pred. No. 6.23e-305;
Matches 497; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 209 tttgattcgtctcaaacccagctggtagcaggagacattgattcctctggcag 268
|||||
QY 355 TGTGATCTGCCTCAAAACCCAGCCCTGGGTAGCAGGAGACCTTGATCTCTGGCAG 414
Db 269 atgaggaaatctctttttctctgcttggaagacagacatgatttgatttcccaag 328
|||||
QY 415 ATGAGAGAAATCTCTTTTCTCTCTTGAAGCAGACAGCTGACTTTGCGATTTGCCAG 474

Db 329 gagagatttggcaaacagctccaaaaggctgaacaccagccctgtcctccatgagatgac 388
|||||
QY 475 GAGGAGCTTGGCAACCCAGTTCCAAAAGGCTGAACCATCCCTGTCTCCATGAGATGATC 534
Db 389 cagcagattctcaatctcttcagcacaagaagtaactcatctgctgttgggatgagaccctc 448
|||||
QY 535 CAGCAGATCTTCAATCTCTTCAGCACAAGGACTCATCTGCTGCTTGGATGACACCTC 594
Db 449 ctagacaattctacactgaactctaccagcagctgaatgacctgggaacctgtgtgata 508
|||||
QY 595 CTAGACAAATTTACACTGAACCTTACCAGCAGCTGAATGACCTGGAGCCTGTGTGATA 654
Db 509 caggggttggggtgacagagactcccctctgatgaaggagactccattctggctgtgagg 568
|||||
QY 655 CAGGGCTGGGGTGCACAGACTCCCTCTGATGAAGGAGACTCCATTCTGCTGTGAGG 714
Db 569 aaatacttccaaagaatcaactctctatctgaaagagaagaataacagcccttgtgctgg 628
|||||
QY 715 AAATACTTCCAAAGAAATCACTCTATCTGAAAGAGAGAAATAGAGCCCTTGTGCTGG 774
Db 629 gaggttgagcagcagaataatcatgagatcttttttctcaacaacttgcagaagaagt 688
|||||
QY 775 GAGGTGTGACAGCAGAAATCATGAGATCTTTTCTTGTCAACAACTTGCAGAAAGT 834
Db 689 ttaagaagtgaagaaatgaaac 710
|||||
QY 835 TTAAGAAGTAAGGAATGATAAC 856
RESULT 12
ID N20005 standard; cDNA; 958 BP.
AC N20005;
DT 18-DEC-1992 (first entry)
DE Hybrid human leukocyte interferon LeIFA.
KW Leukocyte; interferon; antitumor; immunostimulant; virucide; plasmid;
KW plae-IFA.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 61..958
FT /tag= a
PN EP--51873-A.
PD 19-MAY-1982.
PF 09-NOV-1981; 109579.
PR 10-NOV-1980; US-205579.
PR 23-FEB-1981; US-237388.
PR 25-SEP-1981; US-305657.
PA (GENE-) GENENTECH INC.
PI Goeddel DWN;
DR WPI; 82-41788E/21 (41788E).
DR P-PSDB; P20007.
PT Hybrid human leukocyte interferon(s) - useful for treating viral
PT and neoplastic diseases
PS Disclosure; Fig 1; 54pp; English.
CC This hybrid DNA fragment is encoded by the replicable expression
CC vector plasmid plae-IFA and may be expressed in Escherichia coli for
CC production of the peptide. See also N20006-12, N20026-30 and P20008-
CC 14.
SQ Sequence 958 BP; 266 A; 213 C; 191 G; 288 T;
DB 4; Score 492; Match 99.0%; OryMatch 56.6%; Pred. No. 6.23e-305;
Matches 497; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Db 130 tgtgattcgtctcaaacccagctggtagcaggagacattgattgctctctggcag 189

```

Qy 355 TGTGATCTGCCTCAAMCCACGCGCTGGGTAGCAGGAGGACCTTGATGCTCTCGCACAG 414
Db 190 atagagaaatctcttttctctctctggtgaagacagacatgacttttgatttccccag 249
Qy 415 ATGAGAGAATCTCTTTTCTCTCTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474
Db 250 gaggaatttggcaaccagttccaaaggctgaaccatccctgtcctcatgagatgac 309
Qy 475 GAGGAGTTTGGCAACAGTTCAAAAGGCTGAACCACTCCCTGTCTCCATGAGATGATC 534
Db 310 cagcagatcttcaatctctctcagcaaaaggactcatctgtcttgggatgagaccctc 369
Qy 535 CACGAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATGAGACCCCTC 594
Db 370 ctacagaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
Qy 595 CTAGACAAATTTCTACACTGAACCTCTACAGCAGCTCAATGACCTTGGAGCCCTGTGTGATA 654
Db 430 caaggggtggggctgacagagactccctgatgaaggagactccattctggtgtgag 489
Qy 655 CAGGGGCTGGGGCTGACAGACACTCCCTCATGAGGAGGACTCCATTTGCTGCTGAGG 714
Db 490 aataacttccaaagaatcactctctatctgaaagagaagaatacagccctgtgctgg 549
Qy 715 AATATCTTCCAAAGAAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTTGCTCGG 774
Db 550 gaggtgtcagacagaataatcatgagatcttttcttcttgcacaaacttgcaagaaagt 609
Qy 775 GAGCTTGTGACAGCAGCAAAATCATGACATCTTTTCTTGTCAACAACTTGCAGAAAGT 834
Db 610 ttaagaagtaacgaatgaaac 631
Qy 835 TTAAGAAGTAAGCAATGATAC 856

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RESULT 13

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ID N40013 standard; DNA; 503 BP.
AC N40013;
DT 30-NOV-1991 (first entry)
DE DNA encoding recombinant interferon-alpha A.
KW Recombinant interferon-alpha A; ss DNA; antiviral.
FH Key Location/Qualifiers
FT CDS 6
FT /*tag= a
FT misc_feature 12..503
FT /*tag= b
FT /*note= "claimed sequence"
PN EP-128467-A.
PD 19-DEC-1984.
PF 30-MAY-1984; 106214.
PR 01-JUN-1983; US-499964.
PA (HOFF) F Hoffmann-La Roche & Co.
PI DeChiara TM, Tarnowski SJ Jr.
DR WPI; 84-313909/51.
DR P-PSDB; P40022.
PT New antiviral interferon polypeptide(s) free from oligomers - with
PT cysteine residues replaced by other amino acid residues.
PS Disclosure; Fig. 1; 46pp; English.
CC The DNA encodes recombinant interferon-alpha A (rIFN aa). In this
CC protein, Cys 1 may be replaced by a glycine residue, and Cys 98
CC 99 or 100 may be replaced by Ser. These polypeptides have antiviral
CC activity, but unlike prior interferons they are free from
CC oligomers, other than dimers, and they pref. consist of stable

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CC monomers only.
SQ Sequence 503 BP; 144 A; 117 C; 120 G; 122 T;

DB 3; Score 491; Match 99.6%; OryMatch 56.5%; Pred. No. 2,95e-304;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 9 tttgatctgctctcaaacccagcctgggtagcagagagccttggatgctcctggcacag 68
Qy 355 TGTGATCTGCCTCAAMCCACGCGCTGGGTAGCAGGAGGACCTTGATGCTCTCGCACAG 414
Db 69 atagagaaatctcttttctctctggtgaagacagacatgacttttgatttccccag 128
Qy 415 ATGAGAGAATCTCTTTTCTCTCTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474
Db 129 gaggaatttggcaaccagttccaaaggctgaaccatccctgtcctcatgagatgac 188
Qy 475 GAGGAGTTTGGCAACAGTTCAAAAGGCTGAACCACTCCCTGTCTCCATGAGATGATC 534
Db 189 cagcagatcttcaatctctcagcaaaaggactcatctgtctgttgggatgagaccctc 248
Qy 535 CACGAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATGAGACCCCTC 594
Db 249 ctacagaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 308
Qy 595 CTAGACAAATTTCTACACTGAACCTCTACAGCAGCTCAATGACCTTGGAGCCCTGTGTGATA 654
Db 309 caaggggtggggctgacagagactccctgatgaaggagactccattctggtgtgag 368
Qy 655 CAGGGGCTGGGGCTGACAGAGACTCCCTCATGAGGAGGACTCCATTTGCTGCTGAGG 714
Db 369 aataacttccaaagaatcactctctatctgaaagagaagaatacagccctgtgctgg 428
Qy 715 AATATCTTCCAAAGAAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTTGCTCGG 774
Db 429 gaggtgtcagacagaataatcatgagatcttttcttcttgcacaaacttgcaagaaagt 488
Qy 775 GAGCTTGTGACAGCAGCAAAATCATGACATCTTTTCTTGTCAACAACTTGCAGAAAGT 834
Db 489 ttaagaagtaagaa 503
Qy 835 TTAAGAAGTAAGCAA 849

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RESULT 14

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ID 004744 standard; DNA; 573 BP.
AC 004744;
DT 11-OCT-1990 (first entry)
DE Sequence encoding hybrid Hu-IFN alpha A/gamma.
KW Hu-IFN; interferon; tumour; cancer; ds.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..546
FT /*tag= a
FN EP-372707-A.
PD 13-JUN-1990.
PF 27-OCT-1989; 311108.
PR 28-OCT-1989; US-264271.
PA (PEST/) Pestka S.
PI Pestka S;
DR WPI; 90-180507/24.
DR P-PSDB; R05400.
PT Phosphorylated modified proteins, including modified interferon(s) -
PT used in diagnostic and therapeutic applications. eg.
PT pharmacokinetic studies and tumour treatment.

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PS Claim 8; Fig 3; 47pp; English.
 CC Hybrid IFN-gamma and IFN-alpha can be phosphorylated to a high
 CC radio specific activity which IFN-alpha alone cannot.
 CC By introducing phosphorylatable groups, the proteins may be used in
 CC pharmacokinetic studies and diagnostic applications, by attaching 32P
 CC labels to the incorporated sites.
 SQ Sequence 573 BP; 164 A; 130 C; 140 G; 139 T;

DB I; Score 491; Match 99.6%; QryMatch 56.5%; Pred. No. 2.95e-304;
 Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Db 4 tgtgatcgtcctcaaacccacagcctggtagcagagacccttgatcctcctggcacag 63
 Qy 355 TGTGATCGCCTCAAAACCCACAGCGCTGGGTAGCAGGAGGACCTTGATGCTCGGCACAG 414
 Db 64 atgagaaaatctctctttctcctggttgagagacagacatgaatttgattccacag 123
 Qy 415 ATCAGGAGAAATCTCTCTTTCTCCTGCTTGAAGCAGACAGCTGACTTTGGATTTCGCCAG 474
 Db 124 gaggagttggcaaccaggtccaaaggctgaaccatccctgtccctcatgagatgac 183
 Qy 475 GAGGAGTTTGGCAACACAGCTTCCAAAGGCTGAACCATCCCTGCTCCATGAGATGATC 534
 Db 184 cagcagatctcaatctcttcacgacacaaaggactcatctgctgcttgggatgagaccctc 243
 Qy 535 CAGCAGATCTTCAATCTCTTCAAGCAGCAAGGACTCATCTGCTCTGGGATGACACCTC 594
 Db 244 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgata 303
 Qy 595 CTAGACAAATTTACACTGAATCTACCGACGCTGAATGACCTGGAAGCCTGTGTGATA 654
 Db 304 caggggtgggggtgacagagactccctgatgagagagactccattctgctgtgagg 363
 Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGG 714
 Db 364 aaatacttcaagaatactctctatctgaaagagagaaatcacgaccttgctgg 423
 Qy 715 AATACTTCCAGAAATCACTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGG 774
 Db 424 gagggtgcagagcaaatcatgagatcttttcttctgcaacaaacttgcaagaagt 483
 Qy 775 GAGGTGTGACAGCAAAATCATGAGATCTTTTCTTTGTCAACAAACTTCAAGAAAGT 834
 Db 484 ttaagaagtaaggaa 498
 Qy 835 TTAAGAAGTAAGCAA 849

RESULT 15
 ID N20026 standard; DNA; 1109 BP.
 AC N20026;
 DT 18-DEC-1992 (first entry)
 DE Human leukocyte interferon.
 KW Leukocyte; interferon; antitumor; immunostimulant; virucide.
 OS Homo sapiens.
 PN EP--51873-A.
 PD 19-MAY-1982.
 PF 09-NOV-1981; 109579.
 PR 10-NOV-1980; US-205579.
 PR 23-FEB-1981; US-237388.
 PR 25-SEP-1981; US-305657.
 PA (GENE-) GENENTECH INC.
 PI Goeddel DYN;
 DR WPI; 82-41788E/21 (41788E).

PT Hybrid human leukocyte interferon(s) - useful for treating viral
 PT and neoplastic diseases
 PS Disclosure; Fig 9; 54pp; English.
 CC This DNA fragment may be expressed in Escherichia coli for
 CC production of human leukocyte interferon. IFN may be used
 CC for treating viral and neoplastic diseases. See also N20005-12,
 CC N20027-30 and P20007-14.
 SQ Sequence 1109 BP; 307 A; 232 C; 223 G; 347 T;

DB 4; Score 486; Match 99.2%; QryMatch 55.9%; Pred. No. 7.01e-301;
 Matches 500; Conservative 0; Mismatches 2; Indels 2; Gaps 1;
 Db 180 tgtgatcgtcctcaaacccacagcctggtagcagagacccttgatcctcctggcacag 239
 Qy 355 TGTGATCGCCTCAAAACCCACAGCGCTGGGTAGCAGGAGGACCTTGATGCTCGGCACAG 414
 Db 240 atgaggaatctctctttctcctggttgagagacagacatgaatttgattccacag 299
 Qy 415 ATCAGGAGAAATCTCTCTTTCTCCTGCTTGAAGCAGACAGCTGACTTTGGATTTCGCCAG 474
 Db 300 gaggagtttaaggcaaccaggtccaaaggctgaaccatccctgtccctcatgagatga 359
 Qy 475 GAGGAGTTT--GGCAACAGTTCCAAAGGCTGAACCATCCCTGCTCCATGAGATGA 532
 Db 360 tccagcagatctcaatctcttcacgacacaaaggactcatctgctgcttgggatgagacc 419
 Qy 533 TCCAGCAGATCTCAATCTCTTCAAGCAGCAAGGACTCATCTGCTTGGGATGACAGCC 592
 Db 420 tctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgta 479
 Qy 593 TCTAGACAAATTTACACTGAATCTACCGACGCTGAATGACCTGGAAGCCTGTGTGA 652
 Db 480 tacaggggtgggggtgacagagactccctgatgagagagactccattctgctgtga 539
 Qy 653 TACAGGGGTGGGGGTGACAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGA 712
 Db 540 ggaatacttccaaagaatcactctctatctgaaagagagaaatcacgaccttggcct 599
 Qy 713 GGAATACTTCCAAAGAAATCACTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTT 772
 Db 600 gggaggtgtcagagcagaaatcatgagatcttttcttctgcaacaaacttgcaagaaa 659
 Qy 773 GGGAGTTGTACAGCAGCAAAATCATGAGATCTTTTCTTTGTCAACAAACTTCAAGAAA 832
 Db 660 gtttaagaagtaaggaaatgaaac 683
 Qy 833 GTTTAAGAAGTAAGGAATGATAAC 856

Search completed: Tue Aug 29 19:02:12 1995
 Job time : 62 secs.

WATERMAN
(TM)

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MParch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 29 18:49:50 1995; MasPar time 635.43 Seconds
Tabular output not generated. 1006.825 Million cell updates/sec

Title: >US-08-249-671-8
Description: (1:869) from US08249671.seq
Perfect Score: 869
N.A. Sequence: 1 GAATTCGACATTATCGTCAC.....TCATACGATCGTAACGTCA 869
Comp: CTTAAGCTCTAATAGCAGTG.....ACTATTGCTAGCATTGACGT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 493065 seqs, 368106350 bases x 2

Database: emb1-new6

- 1 BCT
- 2 EST1
- 3 EST2
- 4 EST3
- 5 EST4
- 6 EST5
- 7 FUN
- 8 INV1
- 9 INV2
- 10 MAM
- 11 ORG
- 12 PLN
- 13 PRI
- 14 PRO
- 15 ROD
- 16 STS
- 17 SYN
- 18 UNC
- 19 VRT
- 20 VIR

Database: EST
21 EST1
22 EST2
23 EST3
24 EST4
25 EST5

- 26 EST6
- 27 EST7
- 28 EST8
- 29 EST9
- 30 EST10
- 31 EST11
- 32 EST12
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Database: genbank89

- 79 BCT1
- 80 BCT2
- 81 BCT3
- 82 BCT4
- 83 BCT5
- 84 BCT6
- 85 INV1
- 86 INV2
- 87 INV3

88 INV4
89 INV5
90 MAM1
91 MAM2
92 PAT1
93 PAT2
94 PHG
95 PLN1
96 PLN2
97 PLN3
98 PLN4
99 PLN5
100 PLN6
101 PLN7
102 PRI1
103 PRI2
104 PRI3
105 PRI4
106 PRI5
107 PRI6
108 PRI7
109 PRI8
110 PRI9
111 ROD1
112 ROD2
113 ROD3
114 ROD4
115 ROD5
116 ROD6
117 ROD7
118 STR
119 STS1
120 STS2
121 STS3
122 STS4
123 SYN
124 UNA
125 VRL1
126 VRL2
127 VRL3
128 VRL4
129 VRL5
130 VRL6
131 VRT1
132 VRT2
133 VRT3

genbank-new6

Database:

134 BCT
135 EST1
136 EST2
137 EST3
138 EST4
139 EST5
140 EST6
141 EST7
142 EST8
143 INV
144 MAM
145 PHG
146 PLN
147 PRI
148 ROD
149 STS

150 STR
151 SYN
152 UNA
153 VRL
154 VRT

Database: u-emb143.89
155 ALL

Statistics: Mean 11.226; Variance 3.164; scale 3.548

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	498	57.3	589	107	HUMIFNAA2A	Human alpha 2 interfe	0.00e+00
2	498	57.3	1733	107	HUMIFNAA	Human leukocyte inter	0.00e+00
3	498	57.3	1107	93	I01595	Sequence 1 from paten	0.00e+00
4	498	57.3	501	92	A03742	Synthetic gene for in	0.00e+00
5	498	57.3	589	92	A04970	Artificial sequence f	0.00e+00
6	498	57.3	1107	93	I04187	Sequence 8 from paten	0.00e+00
7	498	57.3	742	103	HSIFR6	Human messenger RNA f	0.00e+00
8	498	57.3	784	92	AL2093	oligonucleotide displ	0.00e+00
9	498	57.3	501	93	I01977	Sequence 2 from paten	0.00e+00
10	496	57.1	958	103	HSIFR7	Messenger RNA for hum	0.00e+00
11	496	57.1	941	92	AL5345	Bam HI human interfe	0.00e+00
12	496	57.1	958	93	I01766	Sequence 1 from paten	0.00e+00
13	496	57.1	941	93	I03096	Sequence 8 from paten	0.00e+00
14	496	57.1	961	108	HUMINTAZ	Human interferon-alph	0.00e+00
15	496	57.1	958	93	I04160	Sequence 1 from paten	0.00e+00
16	496	57.1	961	103	HSIFR2	Messenger RNA for hum	0.00e+00
17	494	56.8	506	93	I00069	Sequence 1 from paten	0.00e+00
18	493	56.7	495	92	A04974	Artificial sequence f	0.00e+00
19	491	56.5	573	102	ARHFNAG	Synthetic DNA for Hu-	0.00e+00
20	489	56.3	957	93	I03492	Sequence 1 from paten	0.00e+00
21	486	55.9	1107	93	I07821	Sequence 3 from paten	0.00e+00
22	473	54.4	498	93	I01498	Sequence 1 from paten	0.00e+00
23	469	54.0	490	93	I01473	Sequence 2 from paten	0.00e+00
24	420	48.3	489	93	I07887	Sequence 3 from paten	0.00e+00
25	392	45.1	985	103	HSIFR14	Messenger RNA for hum	0.00e+00
26	392	45.1	985	93	I01788	Sequence 3 from paten	0.00e+00
27	392	45.1	985	93	I03522	Sequence 2 from paten	0.00e+00
28	392	45.1	985	107	HUMIFNAH	Human leukocyte inter	0.00e+00
29	392	45.1	985	93	I04164	Sequence 3 from paten	0.00e+00
30	390	44.9	1544	103	HSIFNA6	Human interferon alph	0.00e+00
31	390	44.9	504	92	A03749	Synthetic gene for in	0.00e+00
32	390	44.9	1126	103	HSIFNA14	Human interferon alph	0.00e+00
33	390	44.9	838	93	I08303	Sequence 1 from paten	0.00e+00
34	390	44.9	504	93	I01985	Sequence 7 from paten	0.00e+00
35	390	44.9	759	93	I08304	Sequence 3 from paten	0.00e+00
36	389	44.8	1069	93	I01598	Sequence 2 from paten	0.00e+00
37	389	44.8	1069	93	I04188	Sequence 9 from paten	0.00e+00
38	389	44.8	1626	103	HSIFD3	Human gene for leukoc	0.00e+00
39	389	44.8	1626	107	HUMIFNAH2	Human leukocyte inter	0.00e+00
40	388	44.6	753	108	HUMINFL	Human leukocyte inter	0.00e+00
41	386	44.4	675	92	AL2652	alpha 88 (IFN alpha)-	0.00e+00
42	386	44.4	1873	103	HSIFD2	Human gene for leukoc	0.00e+00
43	386	44.4	735	103	HSIFR16	Human mRNA for interf	0.00e+00
44	386	44.4	833	93	I08305	Sequence 1 from paten	0.00e+00

45 386 44.4 675 107 HUMFNA Human interferon alph 0.00e+00

ALIGNMENTS

RESULT 1 HUMFNA2A 589 bp DNA PRI 08-NOV-1994
LOCUS Human alpha 2 interferon gene, 3' end.
DEFINITION M29883
ACCESSION
KEYWORDS alpha-interferon; interferon.
SOURCE Human DNA.

ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 1 to 589)
AUTHORS Weber, H. and Weissmann, C.
TITLE Formation of genes coding for hybrid proteins by recombination
between related, cloned genes in E. coli

JOURNAL Nucleic Acids Res. 11 (16), 5661-5669 (1983)

MEDLINE 83299241

COMMENT NCBI gi: 184585

FEATURES Location/Qualifiers

source

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/organism="Homo sapiens"

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/gene="IFNA"

/map="9p22"

/note="alpha 2 interferon; NCBI gi: 386795"

/codon_start=1

/gdb_xref="G00-119-328"

/translation="CDLPQTHSLGSRRTMLLAQMRISLSCIKDRHDFGPQEFQ

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VGVTETPLAKEDSLAVRKYFQITLYIKKKYSPCAWEVVRAEIMRSFSLSTLQES

LRSE"

BASE COUNT 165 a 135 c 135 g 154 t

ORIGIN

DB 107; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 1 tgtgtctgctcaaacccacagctggtagcaggagaccttgatgctctctggcacag 60

Qy 355 TGTGATCTGCCTCAAAACCACAGCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414

Db 61 atgaggagaatctcttttctctgctgctgaaggacagacatgaattggattcccccag 120

Qy 415 ATGAGGAGATCTCTTTCTCTGCTTGAAGGACAGACGCTGCTTGGATTCCCCAG 474

Db 121 gaggagtttgcaacagcttccaaaggctgaacccatccctgtctccatgatgatgc 180

Qy 475 GAGGAGTTGGCAGACAGTTCCAAAGGCTGAAACCATCCTCTCTCATGAGATGATC 534

Db 181 cagcagatctcaatctcttcagcaaaaggactcatctgctgcttgaggatgagaccctc 240

Qy 535 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGGATGAGACCTC 594

Db 241 ctagacaaattctaacatgaactctaccagcagctgaatgaactgagagcctgtgtgata 300

Qy 595 CTAGCAAAATTCTACTGAATCTACCGACGCTGAATGACCTGGAAGCCTGTGTGATA 654

Db 301 cagggggtgggggtgacagagactccctgatgaaggaggactccattctgctgtgagg 360

Qy 655 CAGGGGCTGGGGCTGACAGAGACTCCCTGATGAAGGAGGACTCCATTTCTGGCTGTGAGG 714

Db 361 aaatactccaaagaatcaactctctatctgaagagagaagaatacacagccctgtgctgg 420

Qy 715 AAATACTTCCAAAGATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 774

Db 421 gaggtgtcagagagaatacatgatcttttttcttcttgcacaaacttgcagaagaagt 480

Qy 775 GAGGTGTCTGACAGCAGAAATCATGATCTTTTCTTGTCTCAAAACTTGCAGAAAGT 834

Db 481 ttaagaagtaaggaatgaaac 502

Qy 835 TTAAGAAGTAAGCAATGATAAC 856

RESULT 2

LOCUS HUMFNAA 1733 bp DNA PRI 15-NOV-1994

DEFINITION Human leukocyte interferon (leif) alpha-a gene.

ACCESSION J00207 V00544

KEYWORDS alpha-interferon; interferon.

SOURCE Human cell-line K9-1, cDNA to mRNA and clone Hif-SN206; DNA from

human genomic library of Lawn et al; cDNA to lymphocyte mRNA, clone

202 (see comment).

ORGANISM

Homo sapiens

Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;

Eutheria; Primates; Haplorhini; Catarrhini; Homnidae.

REFERENCE 1 (bases 451 to 1410)

AUTHORS Goeddel, D.V., Yelverton, E., Ullrich, A., Heyneker, H.L., Miorzari, G.,

Holmes, W., Seeburg, P.H., Dull, T.J., May, L., Stebbing, N., Creas, R.,

Maeda, S., McCandless, R., Sloma, A., Tabor, J.M., Gross, M.,

Familletti, P.C. and Pestka, S.

Human leukocyte interferon produced by E. coli is biologically

active

JOURNAL Nature 287 (5781), 411-416 (1980)

MEDLINE 81052322

REFERENCE 2 (bases 659 to 1283)

AUTHORS Maeda, S., McCandless, R., Gross, M., Sloma, A., Familletti, P.C.,

Tabor, J.M., Evinger, M., Levy, W.P. and Pestka, S.

Construction and identification of bacterial plasmids containing

nucleotide sequence for human leukocyte interferon

Proc. Natl. Acad. Sci. U.S.A. 77 (12), 7010-7013 (1980)

MEDLINE 81175079

REFERENCE 3 (bases 529 to 1271)

AUTHORS Streuli, M., Nagata, S. and Weissmann, C.

At least three human type alpha interferons: structure of alpha 2

JOURNAL Science 209 (4463), 1343-1347 (1980)

MEDLINE 81015442

REFERENCE 4 (bases 451 to 1408)

AUTHORS Goeddel, D.V., Leung, D.W., Dull, T.J., Gross, M., Lawn, R.M.,

McCandless, R., Seeburg, P.H., Ullrich, A., Yelverton, E. and Gray, P.W.

The structure of eight distinct cloned human leukocyte interferon

cDNAs

JOURNAL Nature 290 (5801), 20-26 (1981)

MEDLINE 81148795

REFERENCE 5 (bases 1 to 1733)

AUTHORS Lawn, R.M., Gross, M., Houck, C.M., Franke, A.E., Gray, P.V. and

Goeddel, D.V.

DNA sequence of a major human leukocyte interferon gene

Proc. Natl. Acad. Sci. U.S.A. 78 (9), 5435-5439 (1981)

MEDLINE 82060261

REFERENCE 6 (bases 931 to 994)

AUTHORS Bowden, D.W., Mao, J., Gill, T., Hsiao, K., Lillquist, J.S., Testa, D.

and Vovis, G.F.

Cloning of eukaryotic genes in single-strand phage vectors: the

human interferon genes

JOURNAL

Gene 27 (1), 87-99 (1984)

MEDLINE

84183614

COMMENT

IFN-alpha-a is one of at least 13 human leukocyte interferon messages. These sequences represent members of a family of homologous but distinct proteins, some of which may be pseudogenes. IFN-alpha-a codes for a protein having a signal peptide of 23 amino acids and a mature peptide of 165 amino acids, leading to a calculated Mw of 19,390. The sequences denoted alpha-a ([1],[4]) are considered to be from the same gene which encodes sequences denoted alpha-2 ([3],[5]). An interferon protein denoted IFN-alpha-a, which has been sequenced, may not be coded for by this sequence. See other entries for human interferons. Complete source information:

Human cell-line K9-1, cDNA to mRNA [1],[2],[4] and clone Hif-SN206 [3]; DNA from human genomic library of Lawn et al [5]; cDNA to lymphocyte mRNA, clone 202 [6].

NCBI gi: 184581

FEATURES

Location/Qualifiers
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 /organism="Homo sapiens"
 /sequenced_mol="DNA"
 443..1409
 /gene="IFNA"
 /map="9p22"
 /note="alternative; G00-119-328"
 443..1584
 /gene="IFNA"
 /map="9p22"
 /note="alternative; G00-119-328"
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 RRIISFLSKORHDFGPQEEFGNQFOKAETIPVLHEMIQQIFNLFSTKDSNAWDET
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 CAWEVRAEINHSFSLSTNLQESLRSE"
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 /note="G00-119-328"
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 /map="9p22"
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 replace(1109,**)

/gene="IFNA"

/map="9p22"

/citation={1}

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/gene="IFNA"

/map="9p22"

/citation={1}

conflict replace(1351,**)

/gene="IFNA"

/map="9p22"

/citation={4}

conflict

replace(1391,**)

/gene="IFNA"

/map="9p22"

/citation={4}

BASE COUNT 567 a 302 c 328 g 536 t

ORIGIN Chromosome 9p22-pl3; 317 bp upstream of PvuII site.

DB 107; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;

Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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Qy 355 TGTGATCTGCTCAAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCTCCTGGCACAG 414

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Db 640 atgaggagaatctcttttctcctgttgaggacacacatgactttggattcccaag 699

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Qy 415 ATGAGGAATCTCTCTTTCTCTGCTTGAAGCAGACGATGATTTGGATTTCCCCAG 474

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Db 700 gagggattggcaaccagttccaaaaggtgaaaccatccctgtcctccatgagatgac 759

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Qy 475 GAGGAGTTTGGCAACCACTTCCAAAAGGCTGAAACCATCTCTCTCATGATGATGC 534

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Db 760 cagcagatctcaatctcttcagcaaaaggactcatctgtgcttgggatgagaccctc 819

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Qy 535 CAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGCTGCTTGGGATGAGACCTC 594

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Db 820 ctagacaaattctacaatgaactctaccagcagctgaatgaacctggaagcctgtgtgata 879

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Qy 595 CTAGACAAATTTCTACACTGAATCTTACAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654

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Db 880 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 939

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Qy 655 CAGGGGCTGGGGGTGACAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGG 714

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Db 940 aaatactccaagaatcaactctctatctgaaagagaagaatacacgcccttgcctgg 999

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Qy 715 AAATACTTCCAAGAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGG 774

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Qy 775 GAGGTGTGACAGCAGAAAATCATGAGATCTTTTCTTTGTCACAAACTTCACGAAGAGT 834

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Db 1060 ttaagaagtaagaagaataaacaac 1081

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Qy 835 TTAAGAAGTAAGGAATGATAAC 856

RESULT 3

LOCUS 101595 1107 bp ss-DNA

DEFINITION Sequence 1 from patent US 4810645.

ACCESSION 101595

KEYWORDS

SOURCE Unknown.

PAT

05-MAR-1993

ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Goeddel, D.V. and Pestka, S.
TITLE Microbial production of mature human leukocyte interferon K and L
JOURNAL Patent: US 4810645-A 1 07-MAR-1989;
Hoffmann-La Roche Inc.;
Nutley, NJ;
COMMENT NCBI gi: 269892
FEATURES Location/Qualifiers
source 1..1107
/organism="unknown"
BASE COUNT 305 a 232 c 223 g 347 t
ORIGIN

DB 93; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 180 ttgtatgtcctcaaacccacagcctggtagcaggagacctgatgtctctggcacag 239
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Qy 355 TGTGATGTGCTCAACCCACAGCCTGGTAGCAGGAGCCTTGATGCTCGGCACAG 414
Db 240 atgaggagaatctcttttctctgtgtgaaggacacatgaacttttgattccccag 299
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Qy 415 ATGAGGAGAAATCTCTCTTCCTGCTGTGAGGACACAGCTGACTTTGGATTTCCCGAG 474
Db 300 gaggagtttgcaaacaggctcaaaagctgaaccatccctgtctccatgagatgac 359
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Qy 475 GAGGAGTTGGCAACAGTTCCAAAAGGCTCAAAACCATCCCTGTCTCCATGAGATC 534
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Db 480 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 539
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Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATCAAGGAGGAGACTCCATTTGGCTGTGAGG 714
Db 540 aaatacttccaaagaatcactctctatctgaaagagaagaatacagcccttgtgctgg 599
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Qy 715 AAATACTTCCAAGAATCACTCTATCTGAAAGAGAGAAATACAGGCCCTTGTGCTGG 774
Db 600 gaggtgtcagagcagaatcatgatgactttttctttgtccaacaacttgcagaagaagt 659
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Qy 775 GAGGTTGTGAGAGCAGAAATCATGATGATCTTTTCTTTGTCAACAAACTTCCAGAAAGT 834
Db 660 ttaagaagtaaggaatgaaac 681
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Qy 835 TTAAGAGTAGAATGATGAC 856

RESULT 4
LOCUS A03742 501 bp DNA PAT 07-FEB-1994
DEFINITION Synthetic gene for interferon alpha-2(Arg).
ACCESSION A03742
KEYWORDS .
SOURCE unidentified.
ORGANISM unclassified.

REFERENCE 1 (bases 1 to 501)
AUTHORS Hauptmann, R., Sweetly, P., Meindl, P., Guenther, A., Falkner, E.,
Bodo, G. and Maurer-Pogoy, I.
TITLE Hybrid interferons, their use as medicaments and as intermediates
in the preparation of antibodies, their use and process for their
preparation
JOURNAL Patent: EP 0236920-A 2 16-SEP-1987;
COMMENT BOEHRINGER INGELHEIM INTERNATIONAL GmbH
FEATURES NCBI gi: 490340
Location/Qualifiers
source 1..501
/organism="Artificial gene"
CDs 1..501
/note="NCBI gi: 490341"
/product="interferon alpha-2(Arg)"
/translation="MCDLPQTHSLGSRRTMLLAQMRRISLFSCIKDRDFGFPQEEF
GNQPKAETIPVLHEMIQQIFNLFSTKSSAAWDETLLDKFYELYQQLANDLEACVIQ
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SIRSKS"

BASE COUNT 141 a 116 c 123 g 121 t
ORIGIN

DB 92; Score 498; Match 100.0%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db 4 ttgtatgtcctcaaacccacagcctggtagcaggagacctgatgtctctggcacag 63
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Db 64 atgaggagaatctcttttctctgtgtgaaggacacatgaacttttgattccccag 123
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Qy 415 ATGAGGAGAAATCTCTCTTCCTGCTGTGAGGACACAGCTGACTTTGGATTTCCCGAG 474
Db 124 gaggagtttgcaaacaggctcaaaagctgaaccatccctgtctccatgagatgac 183
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Qy 475 GAGGAGTTGGCAACAGTTCCAAAAGGCTCAAAACCATCCCTGTCTCCATGAGATGC 534
Db 184 cagcagatctcaatctcttcagcaaaaggacctatctgctgtgtggatgagaccctc 243
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Qy 535 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCACTGCTGCTGGGATGAGCCCTC 594
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Qy 595 CTAGACAAATTTCACTGACTCTACCGACGCTGAATGACCTGGAGGCTGTGTGATA 654
Db 304 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 363
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Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATCAAGGAGGAGACTCCATTTGGCTGTGAGG 714
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Qy 715 AAATACTTCCAAGAATCACTCTATCTGAAAGAGAGAAATACAGGCCCTTGTGCTGG 774
Db 424 gaggtgtcagagcagaatcatgatgactttttctttgtccaacaacttgcagaagaagt 483
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Qy 775 GAGGTTGTGAGAGCAGAAATCATGATGATCTTTTCTTTGTCAACAAACTTCCAGAAAGT 834
Db 484 ttaagaagtaaggaatga 501
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Qy 835 TTAAGAGTAGAATGATGAC 852

RESULT 5

LOCUS A04970 589 bp DNA PAT 13-JUL-1993
DEFINITION Artificial sequence for interferon-alpha 2.
ACCESSION A04970
KEYWORDS interferon alpha II.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 589)
AUTHORS Weissmann, C. and Weber, H.
TITLE Methods of producing hybrid DNA sequences and hybrid polypeptides
and DNA sequences produced by them
JOURNAL Patent: EP 0141484-A 2 15-MAY-1985;
Biogen, Inc.; BIOGEN, INC
COMMENT NCBI gi: 412536
FEATURES Location/Qualifiers
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/note="NCBI gi: 412537"
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NQFKAEITPVLUHMIQQIFNLFSTKSSANDEFLDKFYELVQQLNDLEACVIQC
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LRSE"
BASE COUNT 165 a 135 c 135 g 154 t
ORIGIN
DB 92; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 1 ttgtatctgctcaaacccacagctgggtacgaggagacattgatctctctggcaag 60
Qy 355 TGTGATCTGCCTCAAAACCCACAGCCTGGGTAGCAGGAGCCTTGATGCTCTGGCACAG 414
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Qy 595 CTAGACAAATTTCTACACTGAATCTTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654
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Qy 775 GAGGTTGTCAAGCGAGAAATCATGAGATCTTTTCTTTTGTTCACAAACTTGCAGAAAGT 834
Db 481 ttaagaagtaaggaatgaaac 502

Qy 835 TTAAGAGTAAGCAATGATAAC 856
RESULT 6
LOCUS I04187 1107 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 8 from patent US 4678751.
ACCESSION I04187
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Goeddel, D.V.
TITLE Hybrid human leukocyte interferons
JOURNAL Patent: US 4678751-A 8 07-JUL-1987;
Genentech, Inc.;
San Francisco, CA;
COMMENT NCBI gi: 268733
FEATURES Location/Qualifiers
source 1..1107
/organism="unknown"
BASE COUNT 305 a 232 c 223 g 347 t
ORIGIN
DB 93; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 180 ttgtatctgctcaaacccacagctgggtacgaggagacattgatctctctggcaag 239
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RESULT 7
LOCUS HSIFR6 742 bp RNA PRI 03-APR-1995
DEFINITION Human messenger RNA for leukocyte (alpha-2) interferon.
ACCESSION V00548
KEYWORDS complementary DNA; interferon; signal peptide.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominoidea.
REFERENCE 1 (bases 1 to 742)
AUTHORS Streuli, M., Nagata, S. and Weissmann, C.
TITLE At least three human type alpha interferons: structure of alpha 2
JOURNAL Science 209 (4463), 1343-1347 (1980)
MEDLINE 81015442
COMMENT NCBI gi: 32740
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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/codon_start=1
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mRNA <1..742
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mat_peptide 52..546
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polya_site 742
/notes="polyA addition site"
BASE COUNT 202 a 170 c 168 g 202 t
ORIGIN
DB 103; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 52 tgtgatctgctcaaacccacagcctgggtgagcaggagccttgatgctcctggcacag 111
Qy 355 TGTGATCTGCTCAAAACCCACAGCGCTGGGTAGCAGGAGACCTTGATGCTCGGCACAG 414
Db 112 atgaagagaatctcttttctctgctgtaagacagacatgaattggatttccccag 171
Qy 415 ATGAGAGAATCTCTCTTTCTCTGCTTTCAGGACAGACGTCACTTTGGATTTCCCGAG 474
Db 172 gaggaattggcaacaggttccaaagctgaaacatccctgtcctccatgatgatc 231
Qy 475 GAGGAGTTTGGCAACGAGTTCCAAAGGCTGAACCATCCCTCTCTCCATGATGATC 534
Db 232 cagcagatcttcaatctcttcacgacaaagactcatctgctgctgggatgagaccctc 291
Qy 535 CAGCAGATCTTCAATCTCTTCAGCAACAAGACTCATCTGCTGCTGGGATGAGACCCCTC 594
Db 292 ctgagcaattctacactgaactctaccacagactgaatgaactgaagcctctgtgata 351
Qy 595 CTAGCAAAATTCTACTGAACCTCTACACAGCTGAATGACCTGGAGCCTCTGTGATA 654
Db 352 caggggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 411
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Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATCAAGGAGGAGCTCCATTTCTCGCTGTGAGG 714
Db 412 aaatacttccaaagaatcactctctatctgaagaagaagaatacagccttctgtgcctgg 471
Qy 715 AAATACTTCCAAAGAAATCACTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGG 774
Db 472 gaggtgtgcagagcagaatcatgatgactcttttctgttgcacaaactgcagaagaagt 531
Qy 775 GAGGTGTGAGAGCAGAAATCATGAGATCTTTTCTTTGTCAACAACTTCAAGAAAGT 834
Db 532 ttaagaagtgaagaatgaaac 553
Qy 835 TTAAGAAGTAAGAAATGATTAAC 856
RESULT 8
LOCUS A12093 784 bp DNA PAT 06-DEC-1993
DEFINITION oligonucleotide displaying a biological or immunological activity
of human interferon.
ACCESSION A12093
KEYWORDS .
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 784)
AUTHORS Weissmann, C.
TITLE DNA sequences, recombinant DNA molecules and processes for
producing human interferon-alpha like polypeptides
JOURNAL Patent: EP 0032134-A 15 15-JUL-1981;
BIOGEN N.V.
COMMENT NCBI gi: 491271
FEATURES
source Location/Qualifiers
CDS <1..563
/notes="NCBI gi: 833176"
/codon_start=2
/product="protein with the immunological activity of human
interferon"
/translation="GGGLLVALLVLISCKSSVCGDLPQTHSLGSRRTLLMLLAQMRRL
ISLFSCLKDRHDFGFPQEEFGNQFQKAETIPVLHEMIQQIENLFSTKDSAAWDETLL
DKFYTELQQQLNDLEACVIGGVGTETPLMKEDSILAVRYKFORITLYLKEKYSPLCA
WEVYRAEIMRSFSLSTNLQESLSRKE"
BASE COUNT 202 a 199 c 181 g 202 t
ORIGIN
DB 92; Score 498; Match 99.6%; QryMatch 57.3%; Pred. No. 0.00e+00;
Matches 500; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 65 tgtgatctgctcaaacccacagcctgggtgagcaggagccttgatgctcctggcacag 124
Qy 355 TGTGATCTGCTCAAAACCCACAGCGCTGGGTAGCAGGAGACCTTGATGCTCGGCACAG 414
Db 125 atgaagagaatctctcttttctctgctgtaagacagacatgaattggatttccccag 184
Qy 415 ATGAGAGAATCTCTCTTTCTCTGCTTTCAGGACAGACGTCACTTTGGATTTCCCGAG 474
Db 185 gaggaattggcaacaggttccaaagctgaaacatccctgtcctccatgatgatc 244
Qy 475 GAGGAGTTTGGCAACGAGTTCCAAAGGCTGAACCATCCCTCTCTCCATGATGATC 534
Db 245 cagcagatcttcaatctcttcacgacaaagactcatctgctgtgggatgagaccctc 304
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QY 535 CACGAGATCTTCAATCTCTTCACGACAAAAGGACTCATCTGCTGCTTGGGATGACAGCCCTC 594

Db 305 ctagacaaattctacactgaactctaccagcagctgaatgaactggaagcctgtgtgata 364
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QY 595 CTAGACAAATTTACACGTAACTCTACACGACGCTGAATGACCTGGAGCCCTGTGTGATA 654

Db 365 cagggggtgggggtgacagagactccccctgatgaagagagactccattctggctgtgaag 424
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QY 655 CAGGGGGTGGGGGTGACAGACACTCCCCGTGATGAGGAGGACTCCATTCTGGCTGTGAGG 714

Db 425 aaatacttccaaagaatacactctctatctgaagagaagaataacagccctgtgctgg 484
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QY 715 AAATATCTTCCAAGAATCACTCTCTATCTGAAGAAGAAATACAGGCCCTTTGTCCTGG 774

Db 485 gaggtgtcagacgagaaatcatgatgactcttttctttgtcaacaacttgcagaagaat 544
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QY 775 GAGCTGTGACAGAGAAATCATGAGATCTTTTCTTGTCAACAACTTGCAGAAAGT 834

Db 545 ttaagaagtaagaatgaaac 566
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QY 835 TTAAGAGTAAGCAATGATAAC 856

RESULT 9

LOCUS I01977 501 bp ss-DNA PAT 05-MAR-1993

DEFINITION Sequence 2 from patent US 4917887.

ACCESSION I01977

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 501)

AUTHORS Hauptmann,R., Swetly,P., Meindl,P., Adolf,G., Falkner,E., Bodo,G. and Maurer-Fogy,I.

TITLE Hybrid interferons, their use as pharmaceutical compositions and as thereof and processes for preparing them

JOURNAL Patent: US 4917887-A 2 17-APR-1990;

Boehringer Ingelheim International GmbH;

DE;

COMMENT NCBI gi: 271078

FEATURES Location/Qualifiers

source 1..501

BASE COUNT 141 a 116 c 123 g 121 t

ORIGIN

DB 93; Score 498; Match 100.0%; QryMatch 57.3%; Pred. No. 0.00e+00;

Matches 498; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 ttgtgctgctcaaacacagcctgggttagcaggagcacttgatcctctggcacag 63
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QY 355 TGTGATCTGCTCAAAACCACAGCCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414

Db 64 atgaagagaatctctctttctctgttgaagacagacgtgaatttgattccccag 123
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QY 415 ATGAGAGAATCTCTTTTCTGCTTGAAGGACAGACGTCACCTTTGGATTCCCGAC 474

Db 124 gagggattggcaacaggttccaaaggtgaaaccatccctgtccatcgatgatc 183
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QY 475 GAGGAGTTGGCAACGATCTCCAAAGGCTGAACATCCCTGCTCTCCATGAGATGATC 534

Db 184 cagcagatcttcaatctcttcagcaacaagagactcatctgctgttgggatgagaccctc 243
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QY 535 CACGAGATCTTCAATCTCTTCACGACAAAAGGACTCATCTGCTGCTTGGGATGACAGCCCTC 594

Db 244 ctagacaaattctacactgaactctaccagcagctgaatgaactggaagcctgtgtgata 303
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QY 595 CTAGACAAATTTACACGTAACTCTACACGACGCTGAATGACCTGGAGCCCTGTGTGATA 654

Db 304 cagggggtgggggtgacagagactccccctgatgaagagagactccattctggctgtgaag 363
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QY 655 CAGGGGGTGGGGGTGACAGACACTCCCCGTGATGAGGAGGACTCCATTCTGGCTGTGAGG 714

Db 364 aaatacttccaaagaatacactctctatctgaagagaagaataacagccctgtgctgg 423
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QY 715 AAATATCTTCCAAGAATCACTCTCTATCTGAAGAAGAAATACAGGCCCTTTGTCCTGG 774

Db 424 gaggtgtcagacgagaaatcatgatgactcttttctttgtcaacaacttgcagaagaat 483
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QY 775 GAGCTGTGACAGAGAAATCATGAGATCTTTTCTTGTCAACAACTTGCAGAAAGT 834

Db 484 ttaagaagtaagaatga 501
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QY 835 TTAAGAGTAAGCAATGA 852

RESULT 10

LOCUS HSIFR7 958 bp RNA PRI 12-SEP-1993

DEFINITION Messenger RNA for human leukocyte (alpha) interferon.

ACCESSION V00549

KEYWORDS complementary DNA; interferon.

SOURCE human.

ORGANISM Homo sapiens

Eukaryotae; mitochondrial eukaryotes; Metazoa/Eumycota group; Metazoa; Eumetazoa; Bilateria; Coelomata; Deuterostomia; Chordata; Vertebrata; Gnathostomata; Osteichthyes; Sarcopterygii; Chonata; Tetrapoda; Amniota; Mammalia; Theria; Eutheria; Archonta; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 958)

AUTHORS Goeddel,D.V., Leung,D.W., Dull,T.J., Gross,M., Lawn,R.M., McCandless,R., Seeburg,P.H., Ullrich,A., Yelverton,E. and Gray,P.W.

TITLE The structure of eight distinct cloned human leukocyte interferon cDNAs

JOURNAL Nature 290 (5801), 20-26 (1981)

MEDLINE 81148795

COMMENT NCBI gi: 32744

FEATURES Location/Qualifiers

source 1..958

/organism="Homo sapiens"

<1..>958

/note="mRNA"

61..627

/note="reading frame (LeIF); NCBI gi: 32745"

/codon start=1

/translation="MALTFALLVALLVLSKSSVCGCDLPQTHSLGSRRTMLLAQM RKISLIFSKLORHDFGPQEEFGNFGKAEIPVLHEMIQQIFNLFSTKDSAAWDET LIDKFYELYQQLNDLEACVIGQVGTETPLAKEDSILAVRKYFORITLYLKEKYSF CAWEYVRAEIMRFSLSLTNLQESLRSE"

BASE COUNT 266 a 211 c 193 g 288 t

ORIGIN

DB 103; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;

Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 ttgtgatctgctcaaacacacagcctgggttagcaggagacaccttgatgctctggcacag 189
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QY 355 TGTGATCTGCTCAAAACCACAGCCCTGGGTAGCAGGAGACCTTTGATGCTCTCGCACAG 414

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Db 190 atqagaaatctctcttctctctgctgaagagacacatgcttggattccccag 249
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Qy 415 ATGAGGAAATCTCTTTCTCTGCTTGGAGGACAGCTGACTTGGATTTCCCGAG 474
Db 250 gaggatttgcaaccagttccaaaggctgaaccatccctgtctccatgagatgac 309
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Qy 475 GAGGATTTGGCAACACAGTTCCAAAAGGCTGAACCATCCCTGCTCCATGAGATGC 534
Db 310 cagcagatcttcaatctcttcagcacaaggactcatctgcttggatgagaccctc 369
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Qy 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGCACTCATCTGCTGCTTGGATGAGACCTC 594
Db 370 ctagacaaattcaactgaactctaccagagctgaatgacctggaagcctgtgtgata 429
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Qy 595 CTAGACAAATTCTACTGACTCTTACCAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654
Db 430 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 489
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Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTCATGAAGGAGGACTCCATTTCTGGCTGTGAGG 714
Db 490 aaatacttccaaagaatcacctctctatctgaagagagaataacagccttgtgctgg 549
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Qy 715 AAATACTTCCAAGAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTGGCTGG 774
Db 550 gaggtgtcagagcagaatcatgatgattctttcttctgtcaacaacttgaagaagt 609
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Qy 775 GAGGTGTGAGAGCAAAATCATGAGATCTTTTCTTTGTCACCAAACTTGCAAGAAAGT 834
Db 610 ttaagaagtaaggaatgaaac 631
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Qy 835 TTAAGAGTAAGCAATGATAAC 856

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RESULT 11
LOCUS A15345 941 bp DNA PAT 27-JAN-1994
DEFINITION Bam H1 human interferon-alpha gene fragment.
ACCESSION A15345

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KEYWORDS
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 941)
AUTHORS Kingman,A.J. and Kingman,S.M.
TITLE Expression vectors
JOURNAL Patent: EP 0073635-A 10 09-MAR-1983;
CELLTECH LIMITED
COMMENT NCBI gi: 491898
FEATURES Location/Qualifiers
source 1..941
/organism="Artificial sequences"
/genes="modified BamH1 human interferon-alpha gene
fragment"
/Note="NCBI gi: 491899"
/codon start=1
/translation="MGCKSSCSVGCGLPQTHSLGSRRTLMLLAQWRKLSLFLKDRH
DFGPPEFGNFOKAETIPVLIHEMIQQIFNLSTKSSAAWDETLLDKFYTLFYQOL
NDLEACVIGQVETPTLMKEDSLAVRKYFORITLYIKKKYSPCAWEVRAELMS
FSLSTNLQESLRKE"
BASE COUNT 315 a 184 c 179 g 263 t
ORIGIN

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DB 92; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;

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Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Db 37 tgtgatctgctcaaacccacagcctgggtagcaggagacacattgatctcctggcacag 96
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Qy 355 TGTATCTGCTCCAAACCCACAGCCTGGGTAGCAGGAGGACTTGTATGCTCTCTGGCAG 414
Db 97 atqaggaataatctctcttctctctgcttgaagacacacatgaacttttgatttcccaag 156
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Qy 415 ATGAGGAAATCTCTTTTCTCTGCTTGAAGGACAGAGCTGACTTTGGATTTCCCGAG 474
Db 157 gaggagttggcaaccaggttccaaaggctgaaccatccctgtctccatgagatgac 216
|||||
Qy 475 GAGGATTTGGCAACACAGTTCCAAAAGGCTGAACCATCCCTGCTCCATGAGATGC 534
Db 217 caqcatcttcaatctcttcagcacaaggactcatctgcttgggatgagaccctc 276
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Qy 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGCACTCATCTGCTTGGATGAGACCTC 594
Db 277 ctagacaaattctacactgaactctaccagagctgaatgacctggaagcctgtgtgata 336
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Qy 595 CTAGACAAATTCTACTGAACTTACGACGACTGAATGACCTTGAAGCCTGTGTGATA 654
Db 337 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 396
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Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTCATGAAGGAGGACTCCATTTCTGGCTGG 714
Db 397 aaatacttccaaagaatcacctctctatctgaagagagaataacagccttgtgctgg 456
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Qy 715 AAATACTTCCAAGAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGG 774
Db 457 gaggtgtcagagcagaatcatgatgattctttcttctgtcaacaacttgaagaagt 516
|||||
Qy 775 GAGGTGTGAGAGCAAAATCATGAGATCTTTTCTTTGTCACCAAACTTGCAAGAAAGT 834
Db 517 ttaagaagtaaggaatgaaac 538
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Qy 835 TTAAGAGTAAGCAATGATAAC 856

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RESULT 12
LOCUS 101766 958 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 1 from patent US 4801685.
ACCESSION 101766
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 958)
AUTHORS Goeddel,D.V. and Pestka,S.
TITLE Microbial production of mature human leukocyte interferon K and L
JOURNAL Patent: US 4801685-A 1 31-JAN-1989;
Hoffmann-La Roche Inc.;
Nutley, NJ;
COMMENT NCBI gi: 269810
FEATURES Location/Qualifiers
source 1..958
/organism="unknown"
BASE COUNT 266 a 211 c 193 g 288 t
ORIGIN

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DB 93; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

- Db 130 tgtgatctgctcaaacccacagctgggtacagaggacattgatctcctggcacag 189
- Qy 355 TGTGATCTGCCTCAAAACCACAGCCTGGGTAGCAGGAGCACCTTGATGCTCTCGGCACAG 414
- Db 190 atgagaaatctctctttctctctgttgagagacacatgaatttgattcccaag 249
- Qy 415 ATGAGGAGAAATCTCTCTTTCTCTCTTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474
Db 250 gaggagttggcaaccagttccaaaaggctgaaaccattccctgtcctccatgagatgac 309
Qy 475 GAGGAGTTTGGCAACAGTTCCAAAAGGCTGAACCACTCCCTGCTCTCCATGAGATGATC 534
Db 310 cagcagattctcaatctctcagcaaaaggactcatctgtctgttgaggatgagaccctc 369
Qy 535 CAGCAGATCTCAATCTCTTCAGCACAAAGACTCATCTGCTGCTTGGGATGAGACCTC 594
Db 370 ctagacaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
Qy 595 CTAGACAAATTTACACTGAACCTTACCAGCAGCTGAATGACCTGGAGAGCCTGTGTGATA 654
Db 430 caggggtgggggtgacagagactccctgatgagaggactccattctggtctgag 489
Qy 655 CAGGGGTGGGGGTGACAGACTCCCTCATGACGAGCACTCCCATTTCTGGCTGTGAGG 714
Db 490 aaatactccaaagaatcaactctctatctgaaagagaagaatacacagccctgtgctgg 549
Qy 715 AAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAAATACAGCCCTTTGTGCTGG 774
Db 550 gaggttgtcagacagaataatcatgagactctttctttgtcaacaacttgcagaagaagt 609
Qy 775 GAGTTGTGACAGCAGAAATCATGACTTTCTTTCTTGTCAACAACTTGCAGAAAGT 834
Db 610 ttaagaagtgaagatgaaac 631
Qy 835 TTAAGAAGTAAGGAATGATAAC 856

RESULT 13
LOCUS I03096 941 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 8 from patent US 4615974.
ACCESSION I03096
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 941)
AUTHORS Kingsman, A.J. and Kingsman, S.M.
TITLE Yeast expression vectors
JOURNAL Patent: US 4615974-A 8 07-OCT-1986;
Celltech Limited;
Berkshire, GB;
COMMENT NCBI gi: 268453
FEATURES
source
location/Qualifiers
1..941
/organism="unknown"
BASE COUNT 315 a 184 c 179 g 263 t
ORIGIN

DB 93; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

- Db 37 tgtgatctgctcaaacccacagctgggtacagaggacattgatctcctggcacag 96
- Qy 355 TGTGATCTGCCTCAAAACCACAGCCTGGGTAGCAGGAGCACTTGATGCTCTCGGCACAG 414

Db 97 atgagaaatctctctttctctctgttgagagacacatgaatttgattcccaag 156
Qy 415 ATGAGGAGAAATCTCTCTTTCTCTCTTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474
Db 157 gaggagttggcaaccagttccaaaaggctgaaaccattccctgtcctccatgagatgac 216
Qy 475 GAGGAGTTTGGCAACAGTTCCAAAAGGCTGAACCACTCCCTGCTCTCCATGAGATGATC 534
Db 217 cagcagattctcaatctctcagcaaaaggactcatctgtctgttgaggatgagaccctc 276
Qy 535 CAGCAGATCTCAATCTCTTCAGCACAAAGACTCATCTGCTGCTTGGGATGAGACCTC 594
Db 277 ctagacaattctcaactgaactctaccagcagctgaatgacctggaagcctgtgtgata 336
Qy 595 CTAGACAAATTTACACTGAACCTTACCAGCAGCTGAATGACCTGGAGCCTGTGTGATA 654
Db 337 caggggtgggggtgacagagactccctgatgagaggactccattctggtctgag 396
Qy 655 CAGGGGTGGGGGTGACAGACTCCCTCATGACGAGCACTCCATTTCTGGCTGTGAGG 714
Db 397 aaatactccaaagaatcaactctctatctgaaagagaagaatacacagccctgtgctgg 456
Qy 715 AAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAAATACAGCCCTTTGTGCTGG 774
Db 457 gaggttgtcagacagaataatcatgagactctttctttgtcaacaacttgcagaagaagt 516
Qy 775 GAGTTGTGACAGCAGAAATCATGACTTTCTTTCTTGTCAACAACTTGCAGAAAGT 834
Db 517 ttaagaagtgaagatgaaac 538
Qy 835 TTAAGAAGTAAGGAATGATAAC 856

RESULT 14
LOCUS HUMINTAZ 961 bp mRNA PRI 06-JAN-1995
DEFINITION Human interferon-alpha mRNA, complete cds.
ACCESSION M54886 M38682
KEYWORDS interferon-alpha.
SOURCE Human leukocyte, cDNA to mRNA.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 961)
AUTHORS Oliver, G., Balbas, P., Valle, F., Soberon, X. and Bolivar, F.
TITLE [Cloning of human leukocyte interferon cDNA and a strategy for its production in E. coli]
JOURNAL Rev. Latinoam. Microbiol. 27 (2), 141-150 (1985)
MEDLINE 86069501
COMMENT NCBI gi: 186498
FEATURES
source
location/Qualifiers
1..961
/organism="Homo sapiens"
/sequenced_mol="cDNA to mRNA"
/tissue type="bone marrow tumor"
61..627
/gene="IFNA"
/map="9p22"
/note="NCBI gi: 186499"
/codon_start=1
/gdb_xref="600-119-328"
/product="interferon"
/translation="MALTFALLVALIVLSKSSSVGCDLPQTHSLGSRRTLLLAQM
RKISLFSCLKORHDFGFPQEEFGNQFQKAETIPVLHEMIQQIFNLFSTKSSAAWDET

LLDKFYTYELIQQIANDLEACVIOGVGVETPIAMKEDSILAVRKIFORITLYIKKKYSP

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BASE COUNT 269 a 211 c 192 g 289 t

ORIGIN

DB 108; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 tgtgactgcctcaaacccacagcctgggtagcaggagacattgatctcctggccacag 189

Qy 355 TGTGATCTGCCTCAAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414

Db 190 atgaagaaatctctcttctctctgcttgaagacagacatgaatttgatttccacag 249

Qy 415 ATGAGGAATCTCTCTTCTCTCTCTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474

Db 250 gaggagttggcaaccagttccaaaggctgaaaccatccctgtcctccatgagatgatc 309

Qy 475 GAGGAGTTGGCAACCACTTCCAAAGGCTCAAAACCATCTCTCTCTCCATGAGATGATC 534

Db 310 cagcagatctcaatctcttcagcaaaaaggactcatctgctgttgggatgagaccctc 369

Qy 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTCTTGGATGAGACCTC 594

Db 370 ctagacaaatctacactgaactctaccagacgtgaatgaacctggaacctgtgtgata 429

Qy 595 CTAGACAAATTTACACTGAACCTTACACAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654

Db 430 cagggggtgggggtgacagagactccctctgatgaaggaggaactccattctggctgtgagg 489

Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGG 714

Db 490 aaatactccaagaatcaactctctatctgaaagagaagaatacacagccttgtgctgg 549

Qy 715 AAATACTTCCAAAGAATCACTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 774

Db 550 gagggtgcagagcaaaatcatgagatcttttcttctgcaacaaacttgcaagaagt 609

Qy 775 GAGGTGTCAGAGCAGAAATCATGATGATCTTTTCTTTGTCAACAACACTTGCAGAAAGT 834

Db 610 ttaagaagtaaggaatgaaac 631

Qy 835 TTAAGAAGTAAGGAATGATAAC 856

RESULT 15

LOCUS I04160 958 bp ss-DNA PAT 05-MAR-1993

DEFINITION Sequence 1 from patent US 4678751.

ACCESSION I04160

KEYWORDS .

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 958)

AUTHORS Goeddel,D.V.

TITLE Hybrid human leukocyte interferons

JOURNAL Patent: US 4678751-A 1 07-JUL-1987;

Genentech, Inc.;

San Francisco, CA;

COMMENT NCBI gi: 268726

FEATURES Location/Qualifiers

source 1..958

/organism="unknown"

BASE COUNT 266 a 211 c 193 g 288 t

ORIGIN

DB 93; Score 496; Match 99.4%; QryMatch 57.1%; Pred. No. 0.00e+00;
Matches 499; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 130 tgtgactgcctcaaacccacagcctgggtagcaggagacattgatctcctggccacag 189

Qy 355 TGTGATCTGCCTCAAAACCCACAGCCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 414

Db 190 atgaagaaatctctcttctctctgcttgaagacagacatgaatttgatttccacag 249

Qy 415 ATGAGGAATCTCTCTTCTCTCTCTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 474

Db 250 gaggagttggcaaccagttccaaaggctgaaaccatccctgtcctccatgagatgatc 309

Qy 475 GAGGAGTTGGCAACCACTTCCAAAGGCTGAAACCATCTCTCTCCATGAGATGATC 534

Db 310 cagcagatctcaatctcttcagcaaaaaggactcatctgctgttgggatgagaccctc 369

Qy 535 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTCTTGGATGAGACCTC 594

Db 370 ctagacaaatctacactgaactctaccagacgtgaatgaacctggaacctgtgtgata 429

Qy 595 CTAGACAAATTTACACTGAACCTTACACAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 654

Db 430 cagggggtgggggtgacagagactccctctgatgaaggaggaactccattctggctgtgagg 489

Qy 655 CAGGGGTGGGGGTGACAGAGACTCCCTGATGAAGGAGGACTCCATTCTGGCTGTGAGG 714

Db 490 aaatactccaagaatcaactctctatctgaaagagaagaatacacagccttgtgctgg 549

Qy 715 AAATACTTCCAAAGAATCACTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 774

Db 550 gagggtgcagagcaaaatcatgagatcttttcttctgcaacaaacttgcaagaagt 609

Qy 775 GAGGTGTCAGAGCAGAAATCATGATGATCTTTTCTTTGTCAACAACACTTGCAGAAAGT 834

Db 610 ttaagaagtaaggaatgaaac 631

Qy 835 TTAAGAAGTAAGGAATGATAAC 856

Search completed: Tue Aug 29 19:00:49 1995

Job time : 659 secs.

WATERBURY (TM)

Release 2.1D John F. Collins, Biocomputing Research Unit.
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MPsrch_nn n.a. - n.a. database search, using Smith-Waterman algorithm

Run on: Tue Aug 29 18:40:42 1995; MasPar time 378.15 Seconds
963.701 Million cell updates/sec

Tabular output not generated.

Title: >US-08-249-671-6
Description: (1:495) from US08249671.seq
Perfect Score: 495
N.A. Sequence: 1 TGTGATCTGCTCAACCCA.....AAAGTTTAAAGAAGTAAGCAA 495
Comp: ACACGTAGACGGAGTTGGGT.....TTTCAAAATCTTCATTCCTT

Scoring table: TABLE default
Gap 6

Nmatch STD : Dbase 0; Query 0

Searched: 493065 seqs, 368106350 bases x 2

Database: emb1-new6

- 1 BCT
- 2 EST1
- 3 EST2
- 4 EST3
- 5 EST4
- 6 EST5
- 7 FUN
- 8 INV1
- 9 INV2
- 10 MAM
- 11 ORG
- 12 PLN
- 13 PRI
- 14 PRO
- 15 ROD
- 16 STS
- 17 SYN
- 18 UNC
- 19 VRT
- 20 VIR

- Database: EST
- 21 EST1
 - 22 EST2
 - 23 EST3
 - 24 EST4
 - 25 EST5

- 26 EST6
- 27 EST7
- 28 EST8
- 29 EST9
- 30 EST10
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Database: genbank89

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- 80 BCT2
- 81 BCT3
- 82 BCT4
- 83 BCT5
- 84 BCT6
- 85 INV1
- 86 INV2
- 87 INV3

88 INV4
89 INV5
90 MAM1
91 MAM2
92 PAT1
93 PAT2
94 PHG
95 PIN1
96 PIN2
97 PIN3
98 PIN4
99 PIN5
100 PIN6
101 PIN7
102 PRI1
103 PRI2
104 PRI3
105 PRI4
106 PRI5
107 PRI6
108 PRI7
109 PRI8
110 PRI9
111 ROD1
112 ROD2
113 ROD3
114 ROD4
115 ROD5
116 ROD6
117 ROD7
118 STR
119 STS1
120 STS2
121 STS3
122 STS4
123 SYN
124 UNA
125 VRL1
126 VRL2
127 VRL3
128 VRL4
129 VRL5
130 VRL6
131 VRT1
132 VRT2
133 VRT3

genbank-new6

134 BCT
135 EST1
136 EST2
137 EST3
138 EST4
139 EST5
140 EST6
141 EST7
142 EST8
143 INV
144 MAM
145 PHG
146 PIN
147 PRI
148 ROD
149 STS

Database:

150 STR
151 SYN
152 UNA
153 VRL
154 VRT
Database: u-emb143_89
155 ALL

Statistics: Mean 10.619; Variance 2.870; scale 3.700

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description	Pred. No.
1	495	100.0	501	92	A03742	Synthetic gene for in	0.00e+00
2	495	100.0	501	93	I01977	Sequence 2 from paten	0.00e+00
3	493	99.6	742	103	HSIFR6	Human messenger RNA f	0.00e+00
4	493	99.6	1107	93	I04187	Sequence 8 from paten	0.00e+00
5	493	99.6	1733	107	HUMIFNAA	Human leukocyte inter	0.00e+00
6	493	99.6	589	107	HUMIFNAA2A	Human alpha 2 interfe	0.00e+00
7	493	99.6	589	92	A04970	Artificial sequence f	0.00e+00
8	493	99.6	784	92	AI2093	oligonucleotide displ	0.00e+00
9	493	99.6	1107	93	I01595	Sequence 1 from paten	0.00e+00
10	493	99.6	495	92	A04974	Artificial sequence f	0.00e+00
11	491	99.2	961	103	HSIFR2	Messenger RNA for hum	0.00e+00
12	491	99.2	961	108	HUMINTAZ	Human interferon-alph	0.00e+00
13	491	99.2	941	92	AI5345	Bam HI human interfer	0.00e+00
14	491	99.2	958	93	I04160	Sequence 1 from paten	0.00e+00
15	491	99.2	958	93	I01766	Sequence 1 from paten	0.00e+00
16	491	99.2	573	102	ARHIFNAG	Synthetic DNA for Hu-	0.00e+00
17	491	99.2	506	93	I00069	Sequence 1 from paten	0.00e+00
18	491	99.2	941	93	I03096	Sequence 8 from paten	0.00e+00
19	491	99.2	958	103	HSIFR7	Messenger RNA for hum	0.00e+00
20	484	97.8	957	93	I03492	Sequence 1 from paten	0.00e+00
21	481	97.2	1107	93	I07821	Sequence 3 from paten	0.00e+00
22	473	95.6	498	93	I01498	Sequence 1 from paten	0.00e+00
23	469	94.7	490	93	I01473	Sequence 2 from paten	0.00e+00
24	419	84.6	489	93	I07887	Sequence 3 from paten	0.00e+00
25	389	78.6	759	93	I08304	Sequence 3 from paten	0.00e+00
26	389	78.6	1544	103	HSIFNA6	Human interferon alph	0.00e+00
27	389	78.6	838	93	I08303	Sequence 1 from paten	0.00e+00
28	388	78.4	985	93	I04164	Sequence 3 from paten	0.00e+00
29	388	78.4	985	93	I03522	Sequence 2 from paten	0.00e+00
30	388	78.4	985	93	I01768	Sequence 3 from paten	0.00e+00
31	388	78.4	985	103	HSIFR14	Messenger RNA for hum	0.00e+00
32	388	78.4	985	107	HUMIFNAH	Human leukocyte inter	0.00e+00
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34	387	78.2	504	93	I01985	Sequence 7 from paten	0.00e+00
35	386	78.0	1126	103	HSIFNA14	Human interferon alph	0.00e+00
36	386	78.0	1626	103	HSIFD3	Human gene for leukoc	0.00e+00
37	386	78.0	1626	107	HUMIFNAH2	Human leukocyte inter	0.00e+00
38	386	78.0	1069	93	I01598	Sequence 2 from paten	0.00e+00
39	386	78.0	1089	93	I04188	Sequence 9 from paten	0.00e+00
40	384	77.6	753	108	HUMINF1	Human leukocyte inter	0.00e+00
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42	383	77.4	735	103	HSIFR16	Human mRNA for interf	0.00e+00
43	383	77.4	736	107	HUMINF	Human leukocyte inter	0.00e+00
44	382	77.2	504	93	A24985	H. sapiens interferon	0.00e+00

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45 382 77.2 675 92 A12652 alpha 88 (IFN alpha). 0.00e+00

ALIGNMENTS

RESULT 1
LOCUS A03742 501 bp DNA PAT 07-FEB-1994
DEFINITION Synthetic gene for interferon alpha-2(Arg) .
ACCESSION A03742
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified
unclassified.
REFERENCE 1 (bases 1 to 501)
AUTHORS Hauptmann,R., Swetly,P., Meindl,P., Guenther,A., Falkner,E.,
Bodo,G. and Maurer-Fogy,I.
TITLE Hybrid Interferons, their use as medicaments and as intermediates
in the preparation of antibodies, their use and process for their
preparation
JOURNAL Patent: EP 0236920-A 2 16-SEP-1987;
BOEHRINGER INGELHEIM INTERNATIONAL GmbH
COMMENT NCBI gi: 490340
FEATURES Location/Qualifiers
source 1..501
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CDS 1..501
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/product="interferon alpha-2(Arg)"
/translaton="MCDLPQTHSLGSRRTLLALLAQMRRIISLFLCKDRDFGFPQEEF
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BASE COUNT 141 a 116 c 123 g 121 t
ORIGIN

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Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ATGAGGAGAATCTCTCTTTTCTCTGCTTGAAGGACAGACGTCGATTTGCCCCAG 120

Db 124 gaggagttggcaaccagttccaaaaggctgaaaccatccctgctccatgagatgac 183
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Db 184 cagcagatcttcaatctcttcagcaaaaggactcatctgctgttggtgagaccctc 243
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Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATCAGACCCCTC 240

Db 244 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 303
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Qy 241 CTAGACAAATTTCTACACTGAACTCTACCAAGCGCTGAATGACCTGGAAGCCTGTGTGATA 300

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Qy 421 GAGGTTGTCAGAGCAGAAATCATGAGATCTTTTCTTCTCAACAAACTTGCAGAAAGT 480
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Qy 481 TTAAGAAGTAAGGAA 495
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RESULT 2
LOCUS 101977 501 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 2 from patent US 4917887.
ACCESSION 101977
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 501)
AUTHORS Hauptmann,R., Swetly,P., Meindl,P., Adolf,G., Falkner,E., Bodo,G.
and Maurer-Fogy,I.
TITLE Hybrid Interferons, their use as pharmaceutical compositions and as
intermediate products for the preparation of antibodies and the use
thereof and processes for preparing them
JOURNAL Patent: US 491787-A 2 17-APR-1990;
Boehringer Ingelheim International GmbH;
DE;
COMMENT NCBI gi: 271078
FEATURES Location/Qualifiers
source 1..501
/organism="unknown"
BASE COUNT 141 a 116 c 123 g 121 t
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DB 93; Score 495; Match 100.0%; QryMatch 100.0%; Pred. No. 0.00e+00;
Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 244 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 303
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Db 304 cagggggtgggggtgacagagactccccctgatgaaggaggactccattctggctgtgagg 363
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Db 484 ttaagaagttaaggaa 498
|||||
Qy 481 TTAAGAAAGTAAGGAA 495
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RESULT 3
LOCUS HSI6R6 742 bp RNA PRI 03-APR-1995
DEFINITION Human messenger RNA for leukocyte (alpha-2) interferon.
ACCESSION V00548
KEYWORDS complementary DNA; interferon; signal peptide.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE 1 (bases 1 to 742)
AUTHORS Streuli,M., Nagata,S. and Weissmann,C.
TITLE At least three human type alpha interferons: structure of alpha 2
JOURNAL Science 209 (4463), 1343-1347 (1980)
MEDLINE 81015442
COMMENT NCBI gi: 32740
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source Location/Qualifiers
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sig_peptide <1..51
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mRNA <1..742
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polyA_site 742
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Db 103; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 1 TCTGATCTGCCTCAACCCAGCGCTGGGTAGCAGGAGCGCTTGATGCTCTGTCACAG 60
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Qy 61 ATGAGGAGAAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGATTTGGATTTCCCGAG 120
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Qy 481 TTAAGAAAGTAAGGAA 495
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RESULT 4
LOCUS I04187 1107 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 8 from patent US 4678751.
ACCESSION I04187
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Goeddel,D.V.
TITLE Hybrid human leukocyte interferons
JOURNAL Patent: US 4678751-A 8 07-JUL-1987;
Genentech, Inc.;
San Francisco, CA;

COMMENT NCBI gi: 268733
FEATURES
source Location/Qualifiers
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Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy 481 TTAGAGACTAAGGAA 495
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RESULT 5 HUMIFNAA 1733 bp DNA PRI 15-NOV-1994
LOCUS Human leukocyte interferon (leif) alpha-a gene.
DEFINITION J00207 V00544
ACCESSION alpha-interferon; interferon.
KEYWORDS Human cell-line Kg-1, cDNA to mRNA and clone Hif-SN206; DNA from
SOURCE human genomic library of Lawn et al; cDNA to lymphocyte mRNA, clone
202 (see comment).

ORGANISM Homo sapiens
Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE 1 (bases 451 to 1410)
AUTHORS Goeddel,D.V., Yelverton,E., Ullrich,A., Heyneker,H.L., Miozzari,G.,
Holmes,M., Seeburg,P.H., Dull,T.J., May,L., Stebbing,N., Crear,R.,
Maeda,S., McCandliis,R., Sloma,A., Tabor,J.M., Grosse,M.,
Familletti,P.C. and Pestka,S.
TITLE Human leukocyte interferon produced by E. coli is biologically
active
JOURNAL Nature 287 (5781), 411-416 (1980)
MEDLINE 81052322
REFERENCE 2 (bases 659 to 1283)
AUTHORS Maeda,S., McCandliis,R., Grosse,M., Sloma,A., Familletti,P.C.,
Tabor,J.M., Evinger,M., Levy,W.P. and Pestka,S.
TITLE Construction and identification of bacterial plasmids containing
nucleotide sequence for human leukocyte interferon
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 77 (12), 7010-7013 (1980)
MEDLINE 81175079
REFERENCE 3 (bases 529 to 1271)
AUTHORS Streuli,M., Nagata,S. and Weissmann,C.
TITLE At least three human type alpha interferons: structure of alpha 2
JOURNAL Science 209 (4463), 1343-1347 (1980)
MEDLINE 81015442
REFERENCE 4 (bases 451 to 1408)
AUTHORS Goeddel,D.V., Leung,D.W., Dull,T.J., Grosse,M., Lawn,R.M.,
McCandliis,R., Seeburg,P.H., Ullrich,A., Yelverton,E. and Gray,P.W.
TITLE The structure of eight distinct cloned human leukocyte interferon
cDNAs
JOURNAL Nature 290 (5801), 20-26 (1981)
MEDLINE 81148795
REFERENCE 5 (bases 1 to 1733)
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AUTHORS Lawn,R.M., Grosse,M., Houck,C.M., Franke,A.E., Gray,P.V. and
Goeddel,D.V.
TITLE DNA sequence of a major human leukocyte interferon gene
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 78 (9), 5435-5439 (1981)
MEDLINE 82060261
REFERENCE 6 (bases 931 to 994)
AUTHORS Bowden,D.W., Mao,J., Gill,T., Hsiao,K., Lillquist,J.S., Testa,D.
and Vovis,G.F.
TITLE Cloning of eukaryotic genes in single-strand phage vectors: the
human interferon genes
JOURNAL Gene 27 (1), 87-99 (1984)
MEDLINE 84183614
COMMENT IFN-alpha-a is one of at least 13 human leukocyte interferon
messages. These sequences represent members of a family of
homologous but distinct proteins, some of which may be pseudogenes.
IFN-alpha-a codes for a protein having a signal peptide of 23 amino
acids and a mature peptide of 165 amino acids, leading to a
calculated Mw of 19,390. The sequences denoted alpha-a (1),[4])
are considered to be from the same gene which encodes sequences
denoted alpha-2 (3),[5]). An interferon protein denoted
IFN-alpha-a, which has been sequenced, may not be coded for by this
sequence. See other entries for human interferons. Complete source
information:
Human cell-line Kg-1, cDNA to mRNA [1],[2],[4] and clone Hif-SN206
[3]; DNA from human genomic library of Lawn et al [5]; cDNA to
lymphocyte mRNA, clone 202 [6].

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conflict replace(451,"")
/gene="IFNA"
/map="9p22"
/citation=[4]
replace(460..462,"")
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/map="9p22"
/citation=[4]
511..579
/gene="IFNA"
/map="9p22"
/note="G00-119-328"
/codon_start=1
511..1077
/gene="IFNA"
/map="9p22"
/note="precursor from leukocyte; NCBI gi: 386793"
/codon_start=1
/gdb_xref="G00-119-328"
/product="interferon alpha-a"
/translation="MALFTALLVALLVLSCKSSCVGCDLPQTHSLCSRRILMLLAQM
RLISFSCIKRHDHFGFQPEFGNQPKAETIPVLHEMIQQIINLFTSKDSAAWDET
LLDKFVTELYQQLNDLEACVIGQGVGTETPLMKEDSILAVRKYFQRIITLYLKEKKYSP
CAWEVRAEINRSFSLSTNIQESIRSE"
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mat_peptide      580..1074
                  /gene="IFNA"
                  /map="9p22"
                  /note="G00-119-328"
                  /codon_start=1
                  /product="interferon alpha-a"
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                  /map="9p22"
                  /citation=[4]
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                  /map="9p22"
                  /citations=[1]
                  replace(1194..1195,**)
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                  /map="9p22"
                  /citations=[1]
                  replace(1351,**)
                  /gene="IFNA"
                  /map="9p22"
                  /citations=[4]
                  replace(1391,**)
                  /gene="IFNA"
                  /map="9p22"
                  /citations=[4]

BASE COUNT      567 a   302 c   328 g   536 t
ORIGIN           Chromosome 9p22-p13; 317 bp upstream of PvuII site.

DB 107; Score    493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 580 tgtgatctgctcaaacccacagcctgggtagcaggaggaccttgatgctcctggcacag 639
|||||
Qy 1 TGTGATCTGCTCAAAACCACAGCTGGGTAGCAGGACGACCTTGATGCTCTCGCACAG 60

Db 640 atgaggagaatctcttttctctgttgaggacagacatgactttggattccccag 699
|||||
Qy 61 ATCAGGAGATCTCTTTCTCTCTGCTTGAAGCAGCAGCTGACTTTGGATTTCCCCAG 120

Db 700 gaggagtttggcaacagcttccaaaaggctgaaccatccctgtcctccatgagatgac 759
|||||
Qy 121 GAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAACACCATCCCTGTCTCCATCAGATGATC 180

Db 760 cagcagatcttcaatctcttcagcaacaaggactcatctgctgctgggatgagaccctc 819
|||||
Qy 181 CAGCAGATCTTCAAATCTCTTCAGCAACAAGGACTCATCTGCTGCTTGGGATCAGACCCCTC 240

Db 820 ctagacaattctacactgaactctaccagcagctgaatgacctggaacctgtgtgata 879
|||||
Qy 241 CTAGACAATTTCTACTGAACTCTTACCAGCAGCTGAATGACCTTGAAGCCTGTGTGATA 300

Db 880 cagggggtgggggtgacagagactccccctgatgaaggaggacctcattctggctgtgagg 939
|||||
Qy 301 CAGGGGGTGGGGGTGACAGAGACTCCCTGATGAAGAGGAGACTCCATCTTGGCTGTGAGG 360

Db 940 aaatacttccaaagaatacacttctctatctgaagagaagaataacagcccttgtgcctgg 999
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Qy 361 AAATACTTCCAAAGAAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTGTGCTGCGTGG 420

Db 1000 gagggtgtcagagcagaataatcatgagatcttttcttttcaacaactgtgcaagaagaagt 1059
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Qy 421 GAGGTTGTTCAGACGAGAAATCATCAGATCTTTTCTTTTGTGCAAAACTTTCAGAAAGT 480
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Db 1060 ttaagaagtaaggaa 1074
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Qy 481 TTAAGAAGTAAGGAA 495

RESULT          6
LOCUS           HUMIFNAZA 589 bp DNA PRI 08-NOV-1994
DEFINITION      Human alpha 2 interferon gene, 3' end.
ACCESSION       M29883
KEYWORDS         alpha-interferon; interferon.
SOURCE          Human DNA.
ORGANISM        Homo sapiens
                Eukaryota; Animalia; Chordata; Vertebrata; Mammalia; Theria;
                Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE       1 (bases 1 to 589)
AUTHORS         Weber, H. and Weissmann, C.
TITLE           Formation of genes coding for hybrid proteins by recombination
                between related, cloned genes in E. coli
JOURNAL         Nucleic Acids Res. 11 (16), 5661-5669 (1983)
MEDLINE         83299241
COMMENT         NCBI gi: 184585
FEATURES         source
                  1..589
                  /organism="Homo sapiens"
                  <1..498
                  /gene="IFNA"
                  /map="9p22"
                  /note="alpha 2 interferon; NCBI gi: 386795"
                  /codon_start=1
                  /gdb_xref="G00-119-328"
                  /translation="CDLPQTHSLGSRRTMLLAQMERISLFSCLKRDHDFGFPQEEFG
                  NFOKAETIPVLHEMIQIENLFSTKSSAAWDETLLDKFYTELYQQLNDLEACVTIQG
                  VGVETPIMKEDSILAVRKYFQRIYLYKEKYSPCAMEWVRAEIMRSFSLSTNIQES
                  LRSKE"
BASE COUNT      165 a   135 c   135 g   154 t
ORIGIN

DB 107; Score    493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tgtgatctgctcaaacccacagcctgggtagcaggaggaccttgatgctcctggcacag 60
|||||
Qy 1 TGTGATCTGCTCAAAACCACAGCTGGGTAGCAGGACGACCTTGATGCTCTCGCACAG 60

Db 61 atgaggagaatctctcttttctctgttgaggacagacatgactttggattccccag 120
|||||
Qy 61 ATCAGGAGATCTCTCTTTCTCTCTGCTTGAAGGACAGACGCTGACTTTGGATTTCCCCAG 120

Db 121 gaggagtttggcaacagcttccaaaaggctgaaccatccctgtcctccatgagatgac 180
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Qy 121 CAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAAGACCATCCCTGTCTCCATCAGATGATC 180

Db 181 cagcagatcttcaatctcttcagcaacaaggactcatctgctgcttgggatgagaccctc 240
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAACAAGGACTCATCTGCTGCTTGGGATGAGACCCCTC 240

Db 241 ctagacaattctacactgaactctaccagcagctgaatgacctgggaacctgtgtgata 300
|||||
Qy 241 CTAGACAATTTCTACTGAACTCTTACCAGCAGCTGAATGACCTTGAAGCCTGTGTGATA 300

Db 301 cagggggtgggggtgacagagactccccctgatgaaggaggacctccattctggctgtgagg 360
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Qy 301 CAGGGGGTGGGGGTGACAGAGACTCCCTGATGAAGAGGAGACTCCATCTTGGCTGTGAGG 360
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Db 361 aaatacttcaagaatacactctctatctgaagaagaataacagcccttgctgag 420
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Qy 361 AATACTTCCAAGAATCACTCTCTATCTGAAGACAGAAATACAGCCCTTGTGCTGG 420
|||||

Db 421 gaggtgtcagacagcaaatcatgagactctttcttctcaacaacttgcaagaagt 480
|||||
Qy 421 GAGGTTGTACAGACAGAAATCATGAGACTCTTTCTTCTCAACAACCTTGCAAGAACT 480
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Db 481 ttaagaagtaaggaa 495
|||||
Qy 481 TTAAGAGTAAGGAA 495
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RESULT 7
LOCUS A04970 589 bp DNA PAT 13-JUL-1993
DEFINITION Artificial sequence for interferon-alpha 2.
ACCESSION A04970
KEYWORDS interferon alpha II.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 589)
AUTHORS Weissmann, C. and Weber, H.
TITLE Methods of producing hybrid DNA sequences and hybrid polypeptides
and DNA sequences produced by them
JOURNAL Patent: EP 0141484-A 2 15-MAY-1985;
Biogen, Inc.; BIOGEN, INC
COMMENT NCBI gi: 412536
FEATURES Location/Qualifiers
source 1..589
/organism="Artificial sequences"
<1..498
/note="NCBI gi: 412537"
/codon_start=1
/product="interferon alpha 2"
/translation="CDLPQTHSLGSRRTMLIAQMRRISLPSCLKRDHDFGFPQEEFG
NQFQKAETIPVLHEMIQOIFNLFSTKDSAAWDETLIDKFYELYQQINDLEACVTQG
VGVETPLMKEDSILAVRKYFORITLYLKEKYSPCMEVRAEIMRSFSLISINQES
IRSK"
BASE COUNT 165 a 135 c 135 g 154 t
ORIGIN

DB 92; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tgtgatctgctcaaacacacagctgggtagcagagaccttgatgctcctggcacag 60
|||||
Qy 1 TGTGATCTGCTCTAAACCCACAGCGCTGGGTAGCAGGACCTTGATGCTCTGGCACAG 60
|||||

Db 61 ataggagaatctctctttctcctgttggaagacagacatgatttgcattccccag 120
|||||
Qy 61 ATGAGGAGATCTCTTTCTCTCTCTGCTTGAAGACAGACGCTTGATTTCCCCAG 120
|||||

Db 121 gagagtttggaacacagttccaaaaggctgaacacatccctgtcctccatgagatgac 180
|||||
Qy 121 GAGGAGTTTGCAACACAGTTCAAAAGGCTGAACACATCCCTGTCTCTCCATGAGATGATC 180
|||||

Db 181 cagcagatcttcaactctctcagcaacaaggactcatctgcttgggagagaccctc 240
|||||
Qy 181 CACGAGATCTCAA TCTCTTCAGCAAAAGGACTCATCTGCTGCTTGGGATGAGACCCCTC 240
|||||

Db 241 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 300
|||||
Qy 241 CTAGACAAATTTCTACACTGAACCTCTACACAGCAGCTGAATGACCTTGGAGCCCTGTGTGATA 300
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Db 301 cagggtgtgggggtgacagactccctctgatgaagagactccattctgctgtgag 360
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Qy 301 CAGGGGTGGGGGTGACAGACTCCCTCTGATGAGGAGACTCCATTCTGGCTGTGAGG 360
|||||

Db 361 aaatacttcaagaatacactctctatctgaagaagaataacagcccttgctgag 420
|||||
Qy 361 AATACTTCCAAGAATCACTCTCTATCTGAAGACAGAAATACAGCCCTTGTGCTGG 420
|||||

Db 421 gaggtgtcagacagcaaatcatgagactctttcttctcaacaacttgcaagaagt 480
|||||
Qy 421 GAGGTTGTACAGACAGAAATCATGAGACTCTTTCTTCTCAACAACCTTGCAAGAACT 480
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Db 481 ttaagaagtaaggaa 495
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Qy 481 TTAAGAGTAAGGAA 495
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RESULT 8
LOCUS A12093 784 bp DNA PAT 06-DEC-1993
DEFINITION oligonucleotide displaying a biological or immunological activity
of human interferon.
ACCESSION A12093
KEYWORDS unidentified.
ORGANISM unidentified.
SOURCE unclassified.
REFERENCE 1 (bases 1 to 784)
AUTHORS Weissmann, C.
TITLE DNA sequences, recombinant DNA molecules and processes for
producing human interferon-alpha like polypeptides
JOURNAL Patent: EP 0032134-A 15 15-JUL-1981;
Biogen N.V
COMMENT NCBI gi: 491271
FEATURES Location/Qualifiers
source 1..784
/organism="Artificial sequences"
<1..563
/note="NCBI gi: 833176"
/codon_start=2
/product="protein with the immunological activity of human
interferon"
BASE COUNT 202 a 199 c 181 g 202 t
ORIGIN

DB 92; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 65 tgtgatctgctcaaacacacagctgggtagcagagaccttgatgctcctggcacag 124
|||||
Qy 1 TGTGATCTGCTCTAAACCCACAGCGCTGGGTAGCAGGACCTTGATGCTCTGGCACAG 60
|||||

Db 125 atgagagaatctctcttctcctgttggaagacagacatgatttgcattccccag 184
|||||
Qy 61 ATGAGGAGATCTCTTTCTCTCTGCTTGAAGACAGACGCTTGATTTCCCCAG 120
|||||

Db 185 gagagatttggaacacagttccaaaaggctgaacacatccctgtcctccatgagatgac 244
|||||
Qy 121 CAGGAGTTTGCAACACAGTTCAAAAGGCTGAACACATCCCTGTCTCTCCATGAGATGATC 180
|||||
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Db 245 cagcagatcttcaatctcttcagcaaaaggactcatctgctgcttgggatgagaccctc 304
|||||
Qy 181 CACGAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATCAGACCCCTC 240
Db 305 ctagacaaattctacactgaactctaccagcagctgaatgacctggaacctgtgtgata 364
|||||
Qy 241 CTAGCAAAATTTACACTGAATCTTACACGAGCTGAATGACCTGGAGCCCTGTGTGATA 300
Db 365 cagggggtgggggtgacagagactccctgatgaaggagactccattctggctgtgagg 424
|||||
Qy 301 CAGGGGGTGGGGGTGACAGACACTCCCTCTGATGAAGGAGGACTCCATTTGCGCTGTGAGG 360
Db 475 aaatactccaagaatacactctctatctgaagaagaatacagcccttgacctgg 484
|||||
Qy 361 AAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCGCTGG 420
Db 485 gaggtgtcagagcaagaatacatgagatcttttcttcttgcacaaacttgcagaagaagt 544
|||||
Qy 421 GAGGTTGTCAGACGACAGAAATCATGAGATCTTTTCTTCTCAACAACCTTGCAAGAAAGT 480
Db 545 ttaagaagtaaggaa 559
|||||
Qy 481 TTAAGAGACTAAGGAA 495

RESULT 9
LOCUS I01595 1107 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 1 from patent US 4810645.
ACCESSION I01595

KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1107)

AUTHORS Goeddel, P. V. and Pestka, S.

TITLE Microbial production of mature human leukocyte interferon K and L
JOURNAL Patent: US 4810645-A 1 07-MAR-1989;
Hoffmann-La Roche Inc.;
Nutley, NJ;

COMMENT NCBI gi: 269892

FEATURES Location/Qualifiers
source 1..1107

/organism="unknown"

BASE COUNT 305 a 232 c 223 g 347 t

ORIGIN

DB 93; Score 493; Match 99.8%; OryMatch 99.68; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 180 tggatctgcctcaaacccacagctgggtagcaggagacattgatctcctggcagcag 239
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Qy 1 TGTGATCTGCTCAAAACCACAGCGCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 240 atgaggagaatctcttcttctcctgcttgaaggacagacatgactttggattccccag 299
|||||
Qy 61 ATGAGGAGAAATCTCTTTCTCTGCTTGAAGGACAGACGCTGATTTGGATTTCCCCAG 120

Db 300 gagaggttggcaaccagttccaaaggctgaaaccatccctgtcctccatgagatgac 359
|||||
Qy 121 GAGGAGTTGGCAACACAGTTCCAAAGGCTGAAACCATCCCTGCTCTCCATCAGATGATC 180

Db 360 cagcagatcttcaatctcttcagcaaaaggactcatctgcttgggatgagaccctc 419
|||||

Qy 181 CACGAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATCAGACCCCTC 240
Db 420 ctagacaaattctacactgaactctaccagcagctgaatgacctggaacctgtgtgata 479
|||||
Qy 241 CTAGCAAAATTTACACTGAATCTTACACGAGCTGAATGACCTGGAAAGCCTGTGTGATA 300
Db 480 cagggggtgggggtgacagagactccctgatgaaggagactccattctggctgtgagg 539
|||||
Qy 301 CAGGGGGTGGGGGTGACAGACACTCCCTCTGATGAAGGAGGACTCCATTTGCGCTGTGAGG 360
Db 540 aaatactccaagaatacactctctatctgaagaagaagaatacagcccttgacctgg 599
|||||
Qy 361 AAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCGCTGG 420
Db 600 gaggtgtcagagcaagaatacatgagatcttttcttcttgcacaaacttgcagaagaagt 659
|||||
Qy 421 GAGGTTGTCAGCAGCAAAATCATGAGATCTTTTCTTCTCAACAACCTTGCAAGAAAGT 480
Db 660 ttaagaagtaaggaa 674
|||||
Qy 481 TTAAGAGACTAAGGAA 495

RESULT 10

LOCUS A04974 495 bp DNA PAT 13-JUL-1993
DEFINITION Artificial sequence for interferon-alpha 2.

ACCESSION A04974

KEYWORDS .

SOURCE unidentified.

ORGANISM unidentified.

REFERENCE 1 (bases 1 to 495)

AUTHORS Weissmann, C. and Weber, H.

TITLE Methods of producing hybrid DNA sequences and hybrid polypeptides
and DNA sequences produced by them

JOURNAL Patent: EP 0141484-A 6 15-MAY-1985;

Biogen, Inc.; BIOGEN, INC

COMMENT NCBI gi: 412540

FEATURES Location/Qualifiers
source 1..495

/organism="Artificial sequences"

BASE COUNT 140 a 116 c 120 g 119 t

ORIGIN

DB 92; Score 493; Match 99.8%; OryMatch 99.68; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tggatctgcctcaaacccacagctgggtagcaggagacattgatctcctggcagcag 60
|||||
Qy 1 TGTGATCTGCTCAAAACCACAGCGCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 61 atgaggagaatctcttcttctcctgcttgaaggacagacatgactttggattccccag 120
|||||
Qy 61 ATGAGGAGAAATCTCTTTTCTCTCTTTGAAGGACAGACGCTGACATTTGGATTTCCCCAG 120

Db 121 gaggaggttggcaaccagttccaaaggctgaaaccatccctgtcctccatgagatgac 180
|||||
Qy 121 GAGGAGTTGGCAACCACTTCCAAAGGCTGAAAGCATCCCTGTCTCTCCATCAGATGATC 180

Db 181 cagcagatcttcaatctcttcagcaaaaggactcatctgcttgggatgagaccctc 240
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGGATCAGACCCCTC 240

Db 241 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 300

CDS 61..627
/gene="IFNA"
/map="9p22"
/note="NCBI gi: 186499"
/codon_start=1
/gdb_xref="G00-119-328"
/product="interferon"
/translation="MALTALLVALLVLSKSSCSVCCDLPQTHSLGSRRTLLMLLAOM
RK1SLFSCIKDRHDFGPQEEFGNOFQKAEIPVLIHMIQOIFNLFSTKSSAAWDET
LLDKFYELYQQLNDLEACVIOGVGTETPLAKEDSILAVRKYFORITLYLKEKRYSP
CAWEVRAEIMRSEFSLSTNIQESLSRSE"
BASE COUNT 269 a 211 c 192 g 289 t
ORIGIN

DB 108; Score 491; Match 99.6%; QryMatch 99.2%; Pred. No. 0.00e+00;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 130 tgtatctgctcaaacaccagcctgggtagcaggaggaccttgatgctctggcacag 189
|||||
Qy 1 TGTGATCTGCTCAAACCCACAGCGCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 60
Db 190 atgagaaaaatctcttttctctgcttgaagcacagacatgactttggatttccccag 249
|||||
Qy 61 ATGAGGAGAAATCTCTCTTCTCTGCTTGAGGACAGACGCTGACTTTCGATTCCCGAG 120
Db 250 gaggagtttgcaaaccaagtccaaaaggctgaaaccatccctgtccctccatgagatgac 309
|||||
Qy 121 GAGGAGTTTGGCAACAGTTCAAAAGGCTGAAACCATCCCTGTCTCCATGAGATGATC 180
Db 310 cagcagatcttcaatctcttcagcaacaaggactcatctgctgtctgggatgagaccctc 369
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGATGAGACCCCTC 240
Db 370 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
|||||
Qy 241 CTAGACAAATTTACACTGAACCTTACACAGCAGCTGAATGACCTTGAAGCCTGTGTGATA 300
Db 430 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggtgtgagg 489
|||||
Qy 301 CAGGGGGTGGGGGTGACAGACTCCCTCTGATGAGGAGGAGACTCCATTCTGGCTGTGAGG 360
Db 490 aaatacttccaaagaatacactctctatctgaagaagaataacagcccttgtgcctgg 549
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Qy 361 AAATACTTCCAAAGAATCACTCTATCTGAAGACAGAGAAATACAGCCCTTGTGCCCTGG 420
Db 550 gagggtgtcagagcagaataatcatgagatcttttctttgtcaacaaacttgcaagaagt 609
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Qy 421 GAGGTTGTGACAGCAGAAATCATGAGATCTTTTCTTCTCAACAAACTTGCAAGAACT 480
Db 610 ttaagaagtaaggaa 624
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Qy 481 TTAAGAAGTAAGGAA 495

RESULT 13
LOCUS A15345 941 bp DNA PAT 27-JAN-1994
DEFINITION Bam HI human interferon-alpha gene fragment.
ACCESSION A15345
KEYWORDS .
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 941)
AUTHORS Kingsman,A.J. and Kingsman,S.M.

TITLE Expression vectors
JOURNAL Patent: EP 0073635-A 10 09-MAR-1983;
CELLTECH LIMITED
COMMENT NCBI gi: 491898
FEATURES
source
Location/Qualifiers
1..941
/organism="Artificial sequences"
7..534
/gene="modified BamHI human interferon-alpha gene
fragment"
/note="NCBI gi: 491899"
/codon_start=1
/translation="MGCKSSCSVCCDLPQTHSLGSRRTLLMLLAOMRKISLFSCLKDRH
DFGPQEEFGNOFQKAEIPVLIHMIQOIFNLFSTKSSAAWDETLLDKFYELYQQL
NDLEACVIOGVGTETPLAKEDSILAVRKYFORITLYLKEKRYSPCAWEVRAEIMRS
FSLSTNIQESLSRSE"
BASE COUNT 315 a 184 c 179 g 263 t
ORIGIN

DB 92; Score 491; Match 99.6%; QryMatch 99.2%; Pred. No. 0.00e+00;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 37 tgtatctgctcaaacaccagcctgggtagcaggaggaccttgatgctctggcacag 96
|||||
Qy 1 TGTGATCTGCTCAAACCCACAGCGCTGGGTAGCAGGAGACCTTGATGCTCTGGCACAG 60
Db 97 atgagaaaaatctcttttctctgcttgaagcacagacatgactttggatttccccag 156
|||||
Qy 61 ATGAGGAGAAATCTCTCTTCTCTGCTTGAGGACAGACGCTGACTTTCGATTTCGCCAG 120
Db 157 gaggagtttgcaaaccaagtccaaaaggctgaaaccatccctgtccctccatgagatgac 216
|||||
Qy 121 GAGGAGTTTGGCAACAGTTCAAAAGGCTGAAACCATCCCTGTCTCCATGAGATGATC 180
Db 217 cagcagatcttcaatctcttcagcaacaaggactcatctgctgtctgggatgagaccctc 276
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTTGGATGAGACCCCTC 240
Db 277 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 336
|||||
Qy 241 CTAGACAAATTTACACTGAACCTTACACAGCAGCTGAATGACCTTGAAGCCTGTGTGATA 300
Db 337 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggtgtgagg 396
|||||
Qy 301 CAGGGGGTGGGGGTGACAGACTCCCTCTGATGAGGAGGAGACTCCATTCTGGCTGTGAGG 360
Db 397 aaatacttccaaagaatacactctctatctgaagaagaataacagcccttgtgcctgg 456
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Qy 361 AAATACTTCCAAAGAATCACTCTATCTGAAGACAGAGAAATACAGCCCTTGTGCCCTGG 420
Db 457 gagggtgtcagagcagaataatcatgagatcttttctttgtcaacaaacttgcaagaagt 516
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Qy 421 GAGGTTGTGACAGCAGAAATCATGAGATCTTTTCTTCTCAACAAACTTGCAAGAACT 480
Db 517 ttaagaagtaaggaa 531
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Qy 481 TTAAGAAGTAAGGAA 495

RESULT 14
LOCUS 104160 958 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 1 from patent US 4678751.
ACCESSION 104160
KEYWORDS .

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 958)
AUTHORS Goeddel, D.V.
TITLE Hybrid human leukocyte interferons
JOURNAL Patent: US 4678751-A 1 07-JUL-1987;
Genentech, Inc.;
San Francisco, CA;
COMMENT NCBI gi: 268726
FEATURES Location/Qualifiers
source I..958
/organism="unknown"
BASE COUNT 266 a 211 c 193 g 288 t
ORIGIN
DB 93; Score 491; Match 99.6%; QryWatch 99.2%; Pred. No. 0.00e+00;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 130 tggatctgcctcaaacccacagcctgggtacgagagaccttgatgctcctggcacag 189
Qy 1 TGTGATCTGCCTCAAAACCCACAGCCTGGGTAGCAGGAGCAGCTTGATGCTCTGCCACAG 60
Db 190 atagagaaatctctcttttctctgttgaggagacacatgactttggattccccag 249
Qy 61 ATGAGGAGAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGATGCTTGGATTTCCCCAG 120
Db 250 gagggatttggcaaccagttccaaaaggctgaaaccatccctgtctccatgagatgac 309
Qy 121 GAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAACCATCCCTGTCTCCATGAGATGATC 180
Db 310 cagcagatcttcaatctcttcagcaaaaggactcatctgctgttgggatgagaccctc 369
Qy 181 CAGCAGATCTTCAATCTCTTACGACAAAGGAGCTCATCTGCTGGGATGAGACCTC 240
Db 370 ctagacaattctacactgaactctaccagagctgaatgacctggaagcctgtgtgata 429
Qy 241 CTAGACAAATTTACACTGAACCTCTACACAGCAGCTGAATGACCTGGAAGCCTCTGTGATA 300
Db 430 cagggggtgggggtgacagagactccctgtgatgaaggagactccattctggctgtgagg 489
Qy 301 CAGGGGTGGGGGTGACAGAGACTCCCTGTATGAAGGAGGAGCTCCATTCTGGCTGTGAGG 360
Db 490 aaatacttccaaagaatcactctctatctgaaagagaagaataacagccctgtgctgg 549
Qy 361 AAATATCTTCCAAAGATCACTCTCTATCTGAAGAGAGAGAAATACAGCCCTTGTGCTGG 420
Db 550 gaggtgtcagagcagaataatcatgagatcttttcttctgtcaacaacttgcaagaaagt 609
Qy 421 GAGGTGTGACAGCAGAAATCATGAGATCTTTTCTTTTGTGCAACAAACTTGCAGAAAGT 480
Db 610 ttaagaagtaaggaa 624
Qy 481 TTAAGAAGTAAGCAA 495

RESULT 15
LOCUS 101766 958 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 1 from patent US 4801685.
ACCESSION 101766
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.
REFERENCE 1 (bases 1 to 958)
AUTHORS Goeddel, D.V. and Pestka, S.
TITLE Microbial production of mature human leukocyte interferon K and L
JOURNAL Patent: US 4801685-A 1 31-JAN-1989;
Hoffmann-La Roche Inc.;
Nutley, NJ;
COMMENT NCBI gi: 269810
FEATURES Location/Qualifiers
source I..958
/organism="unknown"
BASE COUNT 266 a 211 c 193 g 288 t
ORIGIN
DB 93; Score 491; Match 99.6%; QryWatch 99.2%; Pred. No. 0.00e+00;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Db 130 tggatctgcctcaaacccacagcctgggtacgagagaccttgatgctcctggcacag 189
Qy 1 TGTGATCTGCCTCAAAACCCACAGCCTGGGTAGCAGGAGCAGCTTGATGCTCTGCCACAG 60
Db 190 atgaggaataatctctcttttctctgttgaggagacacatgactttggattccccag 249
Qy 61 ATGAGGAGAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGATGCTTGGATTTCCCCAG 120
Db 250 gagggatttggcaaccagttccaaaaggctgaaaccatccctgtctccatgagatgac 309
Qy 121 GAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAACCATCCCTGTCTCCATGAGATGATC 180
Db 310 cagcagatcttcaatctcttcagcaaaaggactcatctgctgttgggatgagaccctc 369
Qy 181 CAGCAGATCTTCAATCTCTTACGACAAAGGAGCTCATCTGCTGGGATGAGACCTC 240
Db 370 ctagacaattctacactgaactctaccagagctgaatgacctggaagcctgtgtgata 429
Qy 241 CTAGACAAATTTACACTGAACCTCTACACAGCAGCTGAATGACCTGGAAGCCTGTGTGATA 300
Db 430 cagggggtgggggtgacagagactccctgtgatgaaggagactccattctggctgtgagg 489
Qy 301 CAGGGGTGGGGGTGACAGAGACTCCCTGTATGAAGGAGGAGCTCCATTCTGGCTGTGAGG 360
Db 490 aaatacttccaaagaatcactctctatctgaaagagaagaataacagccctgtgctgg 549
Qy 361 AAATATCTTCCAAAGATCACTCTCTATCTGAAGAGAGAGAAATACAGCCCTTGTGCTGG 420
Db 550 gaggtgtcagagcagaataatcatgagatcttttcttctgtcaacaacttgcaagaaagt 609
Qy 421 GAGGTGTGACAGCAGAAATCATGAGATCTTTTCTTTTGTGCAACAAACTTGCAGAAAGT 480
Db 610 ttaagaagtaaggaa 624
Qy 481 TTAAGAAGTAAGCAA 495

Search completed: Tue Aug 29 18:47:24 1995
Job time : 402 secs.


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c  #authors  Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
    R.M.; McCandless, R.; Seeburg, P.H.; Ullrich, A.;
    Yelverton, E.; Gray, P.W.
#journal  Nature (1981) 290:20-26
#title  The structure of eight distinct cloned human leukocyte
        interferon cDNAs.
#cross-references MUID:81148795
#accession  D93249
##molecule_type mRNA
##residues  1-188 ##label GO2
##note  eight classes of interferon alpha clones were
        identified; this sequence is derived from class A
REFERENCE  A93888
#authors  Lawn, R.M.; Gross, M.; Houck, C.M.; Franke, A.E.; Gray, P.V.;
        Goeddel, D.V.
#journal  Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5435-5439
#title  DNA sequence of a major human leukocyte interferon gene.
#cross-references MUID:82060261
#accession  A93888
##molecule_type DNA
##residues  1-45,'R',47-188 ##label LAW
##experimental source clone lambda-alpha-2
REFERENCE  A94252
#authors  Streuli, M.; Nagata, S.; Weisemann, C.
#journal  Science (1980) 209:1343-1347
#title  At least three human type alpha interferons: structure of
        alpha2.
#cross-references MUID:81015442
#accession  A94252
##molecule_type mRNA
##residues  7-45,'R',47-188 ##label STR
REFERENCE  A93244
#authors  Wetzel, R.
#journal  Nature (1981) 289:606-607
#title  Assignment of the disulphide bonds of leukocyte interferon.
#cross-references MUID:81123083
#contents  annotation; disulfide bonds
CLASSIFICATION #superfamily interferon alpha
FEATURE  1-23
        #domain signal sequence #status experimental #label StG\
        24-121,52-161 #disulfide_bonds #status experimental
        #length 188 #molecular-weight 21550 #checksum 1790
SUMMARY
DB 2; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 8.11e-178;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 24 cdipqthslgsrrtllmllagmrkislfscldkrdhfgfpqeeqngfkqaeitpvlhemi 83
|||||
Qy 1 CDLPQTHSLGSRRTLLMLLAQMRRIISLFCLEKDRRDFGFPQEEFGNQFQKAETIPVLHEMI 60
|||||
Db 84 qqifnlftkdsaaawdetlldkfyelyqqldleacvlgvgyvtetpinksilavr 143
|||||
Qy 61 QQIFNLFSTKSSAAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120
|||||
Db 144 kyfqrityllylkekkykspcawevvraeimsrfslstnlqeslrsk 188
|||||
Qy 121 KYFQRITLYLKEKKYKSPCAWEVRAEIMRSFSLSTNLQESLSRKE 165
|||||
RESULT 2
ENTRY 2
TITLE 2
ALTERNATE_NAMES 2
ORGANISM 2
#journal  J. Mol. Biol. (1985) 185:227-260
#title  Structural relationship of human interferon alpha genes and
        pseudogenes.
#cross-references MUID:86037205
#accession  A92916
##molecule_type DNA
##residues  1-189 ##label HEN
REFERENCE  A94255
#authors  Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.;
        Ullrich, A.
#journal  Science (1981) 212:1159-1162
#title  DNA sequence of two closely linked human leukocyte interferon
        genes.
#cross-references MUID:81201124
#accession  A94255
##molecule_type DNA
##residues  1-189 ##label LAW

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DATE 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
      27-Jan-1995
ACCESSIONS A25843
REFERENCE  A91374
#authors  Ohara, O.; Teraoka, H.
#journal  FEBS Lett. (1987) 211:78-82
#title  Anomalous behavior of human leukocyte interferon subtypes on
        polyacrylamide gel electrophoresis in the presence of
        dodecyl sulfate.
#cross-references MUID:87105954
#accession  A25843
##molecule_type mRNA
##residues  1-166 ##label ONA
##note  sequence not compared to nucleotide translation
        nucleotide sequence is not given
CLASSIFICATION #superfamily interferon alpha
SUMMARY  #length 166 #molecular-weight 19372 #checksum 7612
DB 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 8.11e-178;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Db 2 cdipqthslgsrrtllmllagmrkislfscldkrdhfgfpqeeqngfkqaeitpvlhemi 61
|||||
Qy 1 CDLPQTHSLGSRRTLLMLLAQMRRIISLFCLEKDRRDFGFPQEEFGNQFQKAETIPVLHEMI 60
|||||
Db 62 qqifnlftkdsaaawdetlldkfyelyqqldleacvlgvgyvtetpinksilavr 121
|||||
Qy 61 QQIFNLFSTKSSAAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120
|||||
Db 122 kyfqrityllylkekkykspcawevvraeimsrfslstnlqeslrsk 166
|||||
Qy 121 KYFQRITLYLKEKKYKSPCAWEVRAEIMRSFSLSTNLQESLSRKE 165
|||||
RESULT 3
ENTRY 3
TITLE 3
ALTERNATE_NAMES 3
ORGANISM 3
DATE 01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
      18-Nov-1994
ACCESSIONS A92916; A94255; B93249; A01834; C23753
REFERENCE  A92916
#authors  Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
        J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
        Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
        Weissmann, C.
#journal  J. Mol. Biol. (1985) 185:227-260
#title  Structural relationship of human interferon alpha genes and
        pseudogenes.
#cross-references MUID:86037205
#accession  A92916
##molecule_type DNA
##residues  1-189 ##label HEN
REFERENCE  A94255
#authors  Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.;
        Ullrich, A.
#journal  Science (1981) 212:1159-1162
#title  DNA sequence of two closely linked human leukocyte interferon
        genes.
#cross-references MUID:81201124
#accession  A94255
##molecule_type DNA
##residues  1-189 ##label LAW

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REFERENCE      A93249
#authors      Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
               R.M.; McCandlies, R.; Seeburg, P.H.; Ullrich, A.;
               Yelverton, E.; Gray, P.W.
#journal      Nature (1981) 290:20-26
#title        The structure of eight distinct cloned human leukocyte
               interferon cDNAs.
#cross-references MUID:81148795
#accession    B93249
               ##molecule_type mRNA
               ##residues 1-174,'F',176-189 ##label GOE
               #note a variant sequence differs from that shown in having the
               175-Phe, 182-Lys, and 184-Gly, the last two being the
               result of a deletion followed by an insertion

GENETICS
#gene         IFNA
#map position 9p22-pl3
CLASSIFICATION #superfamily interferon alpha
KEYWORDS      antiviral
FEATURE
1-23          #domain signal sequence #status predicted #label SIG\
24-189        #product interferon alpha-1-14 #label MAT\
24-122,52-162 #disulfide bonds #status predicted
SUMMARY      #length 189 #molecular-weight 22062 #checksum 2404

DB 2; Score 1050; Match 81.9%; QryMatch 85.9%; Pred. No. 8,45e-151;
Matches 136; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Db 24 cnlsqthlnrrltlmmaqrrisfscldkrdhdfpqeefdgngfkqaaisvlhem 83
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 1 CDLPQTHSLGSRITMLLAQWRISLFSCLKDRDFGFPQEEF-GNQFQAEITPVLHEM 59
mqqtfnlftknsaawdteillekfyieleifqgmndleacvigevgveetplmnedsilav 143
||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 60 IQQIFNLFSYKSDSSAAMDTEILDKFYTEYLQQQINDLEACVIGCVGVTETPLMKESILAV 119

Db 144 kyfqrilylmekyspcavewvraeimsrlsfstnlqkrirkd 189
:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy 120 RYFQRITLYLKKEKYSPCAEWVRAEIMRSFSLSLTWQLQESLRKE 165

RESULT      4
ENTRY
TITLE       D25843 #type complete
ALTERNATE_NAMES
ORGANISM    interferon alpha-G - human
DATE        human leukocyte interferon (IFN)
            #formal name Homo sapiens #common name man
            16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
            27-Jan-1995

ACCESSIONS
REFERENCE    D25843
#authors     Ohara, O.; Teraoka, H.
#journal     FEBS Lett. (1987) 211:78-82
#title       Anomalous behavior of human leukocyte interferon subtypes on
            polyacrylamide gel electrophoresis in the presence of
            dodecyl sulfate.
#cross-references MUID:87105954
#accession   D25843
               ##molecule_type mRNA
               ##residues 1-167 ##label OHA
               #note sequence not compared to nucleotide translation
               #note nucleotide sequence is not given
               #note #superfamily interferon alpha
SUMMARY      #length 167 #molecular-weight 19540 #checksum 57

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[illegible]

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ENTRY          IVHD4B      #type complete
TITLE          interferon alpha-I-4b precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-4b; type I interferon
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
              18-Nov-1994
ACCESSIONS     E23753
REFERENCE      A92916
#authors       Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
              J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
              Schmid, J.; Todokoro, K.; Wachihi, M.; Nagata, S.;
              Weissmann, C.
#journal       J. Mol. Biol. (1985) 185:227-260
#title         Structural relationship of human interferon alpha genes and
              pseudogenes.
#cross-references MUID:86037205
#accession     E23753
#molecule_type DNA
#residues      1-189 #label HEN
GENETICS
#gene          IFNA
#map_position  9p22-p13
CLASSIFICATION #superfamily interferon alpha
KEYWORDS       antiviral
FEATURE
1-23           #domain signal sequence #status predicted #label SIG
24-189         #product interferon alpha-I-4b #label MAT\
24-122,52-162 #disulfide bonds #status predicted
SUMMARY        #length 189 #molecular-weight 21808 #checksum 2553

DB 2; Score 1030; Match 81.3%; QryMatch 84.3%; Pred. No. 1.97e-147;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdlpqtshlgnrralllqagmrspfcldkrdhfgfpqeeefdgqfqtqaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFCIKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstedsaaweqsllekfstelqclndleacviquevgveetplmnydsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYTELQYQQLNDLEACVIOGVGVTEPLMKEDSILAV 119

Db 144 kyqfgritlyltckyspcawevvraeImrslfsltnqlklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFORITLYLKEKYSFPCAMEVVRRAEIMRSFSLSTNLQESLSRKE 165

RESULT 7
ENTRY          IVHUF      #type complete
TITLE          interferon alpha-I-F precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-F; LeIF F; type I interferon
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
              18-Nov-1994
ACCESSIONS     A01832
REFERENCE      A93249
#authors       Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
              R.M.; McCandless, R.; Seeburg, P.H.; Ullrich, A.;
              Yelverton, E.; Gray, P.W.
#journal       Nature (1981) 290:20-26
#title         The structure of eight distinct cloned human leukocyte
              interferon cDNAs.
#cross-references MUID:81148795
#accession     A01832
#molecule_type mRNA

```

```

#residues      1-189 #label GOE
#note          eight classes of interferon alpha clones were
              identified; this sequence is derived from class F
GENETICS
#gene          IFNA
#map_position  9p22-p13
CLASSIFICATION #superfamily interferon alpha
KEYWORDS       antiviral
FEATURE
1-23           #domain signal sequence #status predicted #label SIG
24-189         #product interferon alpha-I-F #label MAT\
24-122,52-162 #disulfide bonds #status predicted
SUMMARY        #length 189 #molecular-weight 21759 #checksum 2746

DB 2; Score 1027; Match 81.9%; QryMatch 84.0%; Pred. No. 6.29e-147;
Matches 136; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Db 24 cdlpqtshlgnrralllqagmrspfcldkrdhfgfpqeeefdgqfqtqaisvlhem 83
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Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFCIKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstedsaaweqsllekfstelqclndleacviquevgveetplmnydsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYTELQYQQLNDLEACVIOGVGVTEPLMKEDSILAV 119

Db 144 kyqfgritlyltckyspcawevvraeImrslfsltnqlklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFORITLYLKEKYSFPCAMEVVRRAEIMRSFSLSTNLQESLSRKE 165

RESULT 8
ENTRY          E25843      #type complete
TITLE          interferon alpha-F - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM       #formal_name Homo sapiens #common_name man
DATE           16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
              27-Jan-1995
ACCESSIONS     E25843
REFERENCE      A91374
#authors       Ohara, O.; Teraoka, H.
#journal       FEBS Lett. (1987) 211:78-82
#title         Anomalous behavior of human leukocyte interferon subtypes on
              polyacrylamide gel electrophoresis in the presence of
              dodecyl sulfate.
#cross-references MUID:87105954
#accession     E25843
#molecule_type mRNA
#residues      1-167 #label OHA
#note          sequence not compared to nucleotide translation
              nucleotide sequence is not given
#note          #superfamily interferon alpha
CLASSIFICATION #length 167 #molecular-weight 19461 #checksum 9875
SUMMARY

DB 4; Score 1027; Match 81.9%; QryMatch 84.0%; Pred. No. 6.29e-147;
Matches 136; Conservative 16; Mismatches 13; Indels 1; Gaps 1;

Db 2 cdlpqtshlgnrralllqagmrspfcldkrdhfgfpqeeefdgqfqtqaisvlhem 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFCIKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 62 iqqtfnlfstedsaaweqsllekfstelqclndleacviquevgveetplmnydsilav 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKSSAAWDETLLDKFYTELQYQQLNDLEACVIOGVGVTEPLMKEDSILAV 119

```

```

Db 122 kkyfqrtilytkkyspcawevvraeimsrfsfslkfqrllrke 167
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Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRSFSLTNLQESLSRKE 165

RESULT 9
ENTRY
TITLE
ALTERNATE_NAMES
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:85229953
#accession
#molecule_type mRNA
#residues 1-189 ##label M12
CLASSIFICATION #superfamily interferon alpha
FEATURE
24-189
#product interferon alpha-I' #label MAT
#length 189 #molecular-weight 21728 #checksum 2510

DB 4; Score 1026; Match 81.3%; OryMatch 84.0%; Pred. No. 9.26e-147;
Matches 135; Conservative 19; Mismatches 11; Indels 1; Gaps 1;

Db 24 cdllpqtshlgnrrallilaqmgrisfscldkrdhfglqpqeefdngfqtgaisvlhem 83
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Qy 1 CDLPQTHSIGSRRTMLLAQMRRLISLSCIKDRDRDFGFPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqtfnlfstedsaawdelldkfytelyqqlndleacvlgvgvteplmkedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 IQQIFNLSTKDSAAWDELTDKFTELYQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsrfsfsltnlqltklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRSFSLTNLQESLSRKE 165

RESULT 10
ENTRY
TITLE
ALTERNATE_NAMES
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:86037205
#accession
#molecule_type DNA
#residues 1-189 ##label HEN
GENETICS
#gene IFNA

IVHU16 #type complete
interferon alpha-I-16 precursor - human
HUIFN-alpha-I-16; type I interferon
#formal_name Homo sapiens #common_name man
28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
18-Nov-1994
G23753
A92916
Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambach, A.;
Schmid, J.; Tokoro, K.; Walchli, M.; Nagata, S.;
Weissmann, C.
J. Mol. Biol. (1985) 185:227-260
#title Structural relationship of human interferon alpha genes and
pseudogenes.
#cross-references MUID:86037205
#accession G23753
#molecule_type DNA
#residues 1-189 ##label HEN
IFNA

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#map_position 9p22-pl3
CLASSIFICATION #superfamily interferon alpha
KEYWORDS antiviral
FEATURE
1-23
#domain signal sequence #status predicted #label SIG\
24-189
#product interferon alpha-I-16 #label MAT\
24-122,52-162
#disulfide_bonds #status predicted
SUMMARY
#length 189 #molecular-weight 21711 #checksum 45

DB 2; Score 1025; Match 82.5%; OryMatch 83.9%; Pred. No. 1.36e-146;
Matches 137; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Db 24 cdllpqtshlgnrrallilaqmgrisfscldkrdyfgfpqevfdngfqkaaisafhem 83
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Qy 1 CDLPQTHSIGSRRTMLLAQMRRLISLSCIKDRDRDFGFPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqtfnlfstedsaawdelldkfytelyqqlndleacvlgvgvteplmkedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 IQQIFNLSTKDSAAWDELTDKFTELYQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsrfsfsltnlqltklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRSFSLTNLQESLSRKE 165

RESULT 11
ENTRY
TITLE
ORGANISM
DATE
ACCESSIONS
REFERENCE
#authors
#journal
#title
#cross-references MUID:85038533
#accession
#status preliminary
#molecule_type DNA
#residues 1-189 ##label TOR
CLASSIFICATION #superfamily interferon alpha
SUMMARY
#length 189 #molecular-weight 21711 #checksum 45

DB 4; Score 1025; Match 82.5%; OryMatch 83.9%; Pred. No. 1.36e-146;
Matches 137; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Db 24 cdllpqtshlgnrrallilaqmgrisfscldkrdyfgfpqevfdngfqkaaisafhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 1 CDLPQTHSIGSRRTMLLAQMRRLISLSCIKDRDRDFGFPQEEF-GNQFQKAEITPVLHEM 59

Db 84 iqqtfnlfstedsaawdelldkfytelyqqlndleacvlgvgvteplmkedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 60 IQQIFNLSTKDSAAWDELTDKFTELYQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsrfsfsltnlqltklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRSFSLTNLQESLSRKE 165

RESULT 12
ENTRY
TITLE

```

```

* ORGANISM      #formal_name Homo sapiens #common_name man
  DATE          01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
                30-Sep-1993
ACCESSIONS      A01835
REFERENCE        A94255
#authors        Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.;
                Ullrich, A.
#journal        Science (1981) 212:1159-1162
#title          DNA sequence of two closely linked human leukocyte interferon
                genes.
#cross-references MUID:81201124
#accession      A01835
#molecule_type DNA
#residues       1-189 ##label LAW
#note           residues 1-23 correspond to the signal sequence
CLASSIFICATION  #superfamily interferon alpha
SUMMARY         #length 189 #molecular-weight 21698 #checksum 2966

DB 2; Score     1023; Match 81.3%; OryMatch 83.7%; Pred. No. 2.96e-146;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdllpqtshlnrralllqgmgrispfscldrdpqlpqeefdnqfqtqaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSIGSRRTLLLAQMRRLISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlstdessaaweqsllekfstelyqqlnleacviquevgveetplmnedslav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLDDKFEYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkerkyspcawevvraeimrslsfstnlqklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVVRRAEIMRFSLSLSTNLQESLSRKE 165

RESULT 13
ENTRY    IVHWA5          #type complete
TITLE    interferon alpha-5 precursor - human
ORGANISM #formal_name Homo sapiens #common_name man
DATE     01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
                18-Nov-1994
ACCESSIONS A60937; A01830
REFERENCE  A60937
#authors   Bartholomew, C.; Windass, J.D.
#journal   J. Interferon Res. (1989) 9:407-417
#title     Identification of a functional allele of a human
            interferon-alpha gene previously characterized as a
            pseudogene.
#accession A60937
#molecule_type DNA
#residues  1-189 ##label BAR
#note      this genomic sequence, SMTIII.1A, encodes a functional
            allele for alpha interferon at the locus pseudo-Leif-L
            that, in other allelic forms, contains a stop codon at
            the end of the signal sequence and is a pseudogene.

REFERENCE  A93249
#authors   Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
            R.M.; McCandlies, R.; Seeburg, P.H.; Ullrich, A.;
            Yelverton, E.; Gray, P.W.
#journal   Nature (1981) 290:20-26
#title     The structure of eight distinct cloned human leukocyte
            interferon cDNAs.
#cross-references MUID:81148795
#accession  A01830
#molecule_type mRNA

```

```

#residues       1-189 ##label GOE
#note           eight classes of interferon alpha clones were
                identified; this sequence is derived from class C
CLASSIFICATION  #superfamily interferon alpha
FEATURE         1-23
SUMMARY         #domain signal sequence #status predicted #label SIG
                #length 189 #molecular-weight 21835 #checksum 2522

DB 2; Score     1017; Match 81.3%; OryMatch 83.2%; Pred. No. 3.03e-145;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdllpqtshlnrralllqgmgrispfscldrdhfrfpqeednqfqtqaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSIGSRRTLLLAQMRRLISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlstdessaaweqsllekfstelyqqlnleacviquevgveetplmnedslav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLDDKFEYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkerkyspcawevvraeimrslsfstnlqklrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVVRRAEIMRFSLSLSTNLQESLSRKE 165

RESULT 14
ENTRY    F25843          #type complete
TITLE    interferon alpha-J - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM  #formal_name Homo sapiens #common_name man
DATE     16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
                27-Jan-1995
ACCESSIONS F25843
REFERENCE  A91374
#authors   Ohara, O.; Teraoka, H.
#journal   FEBS Lett. (1987) 211:78-82
#title     Anomalous behavior of human leukocyte interferon subtypes on
            polyacrylamide gel electrophoresis in the presence of
            dodecyl sulfate.
#cross-references MUID:87105954
#accession  F25843
#molecule_type mRNA
#residues  1-167 ##label OHA
#note      sequence not compared to nucleotide translation
            nucleotide sequence is not given
#note      nucleotide sequence is not given
CLASSIFICATION #superfamily interferon alpha
SUMMARY         #length 167 #molecular-weight 19737 #checksum 451

DB 4; Score     1012; Match 79.5%; OryMatch 82.8%; Pred. No. 2.10e-144;
Matches 132; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

Db 2 cdllpqtshlnrralllqgmgrispfscldrdhfrfpqeednqfqtqaisvlhem 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSIGSRRTLLLAQMRRLISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 62 iqqtfnlstdessaaweqsllekfstelyqqlnleacviquevgveetplmnedfilav 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLDDKFEYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119

Db 122 rkyfqrtilytkerkyspcawevvraeimrslsfstnlqklrrkd 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVVRRAEIMRFSLSLSTNLQESLSRKE 165

RESULT 15

```



```
* ENTRY          IVRU18      #type complete
* TITLE          interferon alpha-I-8 precursor - human
* ALTERNATE_NAMES HuIFN-alpha-I-8; type I interferon
* ORGANISM       #formal_name Homo sapiens #common_name man
* DATE           28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
                  18-Nov-1994
ACCESSIONS       D23753
REFERENCE        A92916
#authors        Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
                  J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
                  Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
                  Weissmann, C.
#journal         J. Mol. Biol. (1985) 185:227-260
#title          Structural relationship of human interferon alpha genes and
                  pseudogenes.
#cross-references MUID:86037205
#accession       D23753
#molecule_type  DNA
#residues        1-189 ##label HEN
GENETICS
#gene            IFNA
#map_position     9p22-pl3
CLASSIFICATION   #superfamily interferon alpha
KEYWORDS         antiviral
FEATURE
  1-23            #domain signal sequence #status predicted #label SIG\
  24-189          #product interferon alpha-I-8 #label MAT\
  24-122,52-162   #disulfide_bonds #status predicted
SUMMARY          #length 189 #molecular_weight 21989 #checksum 1052
DB 2; Score      1012; Match 82.5%; OryMatch 82.8%; Pred. No. 2.10e-144;
Matches 137; Conservative 13; Mismatches 15; Indels 1; Gaps 1;
Db 24 cdlpgtshlgmrllagmrripfscldkrdhdfpqeefddkqfkaqaisvlhem 83
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 1 CDLPQTHSLGSRRTYLLAQMRRLSLFSCIKDREDFGFPQEEFGN-QFOAETIPVLHEM 59
Db 84 iqqtnlftskdsaalddetlldfyieldqqndlscvmqevqviesplmysdsilav 143
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 60 IQQIFNLFSTKSSAAWDETLDDKFTELYQQQLNDLEACVIGGVGVETPIMKEDSILAV 119
Db 144 rkyfqrtilylekkysscawevvraeimrfsislndqlrlske 189
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
QY 120 RKYFQRITLYLKEKYSPCAEVWVRAEIMRFSISLTNIQESILRSKE 165
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Search completed: Tue Aug 29 17:06:58 1995
Job time : 22 secs.


```

#authors      Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
              R.M.; McCandliss, R.; Seeburg, P.H.; Ullrich, A.;
              Yelverton, E.; Gray, P.W.
#journal      Nature (1981) 290:20-26
#title        The structure of eight distinct cloned human leukocyte
              interferon cDNAs.
#cross-references MUID:81148795
#accession     D93249
##molecule_type mRNA
##residues     1-188 ##label G02
##note         eight classes of interferon alpha clones were
              identified; this sequence is derived from class A
REFERENCE      A93888
#authors      Lawn, R.M.; Gross, M.; Houck, C.M.; Franke, A.E.; Gray, P.V.;
              Goeddel, D.V.
#journal      Proc. Natl. Acad. Sci. U.S.A. (1981) 78:5435-5439
#title        DNA sequence of a major human leukocyte interferon gene.
#cross-references MUID:82060261
#accession     A93888
##molecule_type DNA
##residues     1-45, 'R', 47-188 ##label LAW
##experimental source clone lambda-alpha-2
REFERENCE      A94252
#authors      Streuli, M.; Nagata, S.; Weissmann, C.
#journal      Science (1980) 209:1343-1347
#title        At least three human type alpha interferons: structure of
              alpha2.
#cross-references MUID:81015442
#accession     A94252
##molecule_type mRNA
##residues     7-45, 'R', 47-188 ##label STR
REFERENCE      A93244
#authors      Wetzel, R.
#journal      Nature (1981) 289:606-607
#title        Assignment of the disulphide bonds of leukocyte interferon.
#cross-references MUID:81123083
#contents      annotation; disulfide bonds
CLASSIFICATION #superfamily interferon alpha
FEATURE        1-23
              24-121,52-161
              #domain signal sequence #status experimental #label SIG
              #disulfide bonds #status experimental
SUMMARY        #length 188 #molecular-weight 21550 #checksum 1790
              #length 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdlpqtshlgrrtllmlagmrkislscldkrdhdfqpeefgnqfkaetipvlhemi 83
      |||||||
      1 CDLPQTHSGSRRTLLMLAQMRRIISLFCIKDRDFFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 84 qqifnlfskdsaaawdetlldkfyelyqqldleacvlgvgvgtetplmkedsilavr 143
      |||||||
      61 QQIFNLFSTKDSNAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120

Db 144 kyfgritlylkekyspcawevvraeimsrfsfstnlqeslrsk 188
      |||||||
      121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

Qy 121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 2
ENTRY   A25843
TITLE   Interferon alpha-A - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM #formal_name Homo sapiens #common_name man
CLASSIFICATION #superfamily interferon alpha
FEATURE    1-23
            24-121,52-161
            #domain signal sequence #status experimental #label SIG
            #disulfide bonds #status experimental
SUMMARY    #length 188 #molecular-weight 21550 #checksum 1790
            #length 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 8.11e-178;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 24 cdlpqtshlgrrtllmlagmrkislscldkrdhdfqpeefgnqfkaetipvlhemi 83
      |||||||
      1 CDLPQTHSGSRRTLLMLAQMRRIISLFCIKDRDFFGFPQEEFGNQFQKAETIPVLHEMI 60

Qy 1 CDLPQTHSGSRRTLLMLAQMRRIISLFCIKDRDFFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 84 qqifnlfskdsaaawdetlldkfyelyqqldleacvlgvgvgtetplmkedsilavr 143
      |||||||
      61 QQIFNLFSTKDSNAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120

Qy 61 QQIFNLFSTKDSNAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120

Db 144 kyfgritlylkekyspcawevvraeimsrfsfstnlqeslrsk 188
      |||||||
      121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

Qy 121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 2
ENTRY   A25843
TITLE   Interferon alpha-A - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM #formal_name Homo sapiens #common_name man

```

```

DATE          16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
              27-Jan-1995
ACCESSIONS    A25843
REFERENCE     A91374
#authors      Ohara, O.; Teraoka, H.
#journal      FEBS Lett. (1987) 211:78-82
#title        Anomalous behavior of human leukocyte interferon subtypes on
              polyacrylamide gel electrophoresis in the presence of
              dodecyl sulfate.
#cross-references MUID:87105954
#accession     A25843
##molecule_type mRNA
##residues     1-166 ##label OHA
##note         sequence not compared to nucleotide translation
              nucleotide sequence is not given
##note         #superfamily interferon alpha
CLASSIFICATION #length 166 #molecular-weight 19372 #checksum 7612
SUMMARY

Db 4; Score 1210; Match 98.8%; QryMatch 99.0%; Pred. No. 8.11e-178;
Matches 163; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Db 2 cdlpqtshlgrrtllmlagmrkislscldkrdhdfqpeefgnqfkaetipvlhemi 61
      |||||||
      1 CDLPQTHSGSRRTLLMLAQMRRIISLFCIKDRDFFGFPQEEFGNQFQKAETIPVLHEMI 60

Qy 1 CDLPQTHSGSRRTLLMLAQMRRIISLFCIKDRDFFGFPQEEFGNQFQKAETIPVLHEMI 60

Db 62 qqifnlfskdsaaawdetlldkfyelyqqldleacvlgvgvgtetplmkedsilavr 121
      |||||||
      61 QQIFNLFSTKDSNAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120

Qy 61 QQIFNLFSTKDSNAWDETLLDKFYELYQQLDLEACVIGVGVTETPLMKEDSILAVR 120

Db 122 kyfgritlylkekyspcawevvraeimsrfsfstnlqeslrsk 166
      |||||||
      121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

Qy 121 KYFORITLYLKEKYSPCAWEVVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 3
ENTRY   IVHU14
TITLE   Interferon alpha-I-14 precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-14; lambda-2-h; type I interferon
ORGANISM #formal_name Homo sapiens #common_name man
DATE      01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
              18-Nov-1994
ACCESSIONS    A92916; A94255; B93249; A01834; C23753
REFERENCE     A92916
#authors      Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
              J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
              Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
              Weissmann, C.
#journal      J. Mol. Biol. (1985) 185:227-260
#title        Structural relationship of human interferon alpha genes and
              pseudogenes.
#cross-references MUID:86037205
#accession     A92916
##molecule_type DNA
##residues     1-189 ##label HEN
REFERENCE     A94255
#authors      Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.;
              Ullrich, A.
#journal      Science (1981) 212:1159-1162
#title        DNA sequence of two closely linked human leukocyte interferon
              genes.
#cross-references MUID:81201124
#accession     A94255
##molecule_type DNA
##residues     1-189 ##label LAW

```

```

REFERENCE      A93249
#authors      Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Grosse, M.; Lawn,
               R.M.; McCandless, R.; Seeburg, P.H.; Ullrich, A.;
               Yelverton, E.; Gray, P.W.
#journal      Nature (1981) 290:20-26
#title        The structure of eight distinct cloned human leukocyte
               interferon cDNAs.
#cross-references MUID:81148795
#accession    B93249
#molecule_type mRNA
#residues     1-174, F', 176-189 ##label GOE
#note         a variant sequence differs from that shown in having
               175-Phe, 182-Iys, and 184-Gly, the last two being the
               result of a deletion followed by an insertion

GENETICS
#gene         IFNA
#map_position 9p22-p13
CLASSIFICATION #superfamily interferon alpha
KEYWORDS      antiviral
FEATURE
  1-23        #domain signal sequence #status predicted #label SIG\
  24-189      #product interferon alpha-I-14 #label MAT\
  24-122,52-162 #disulfide bonds #status predicted
SUMMARY       #length 189 #molecular-weight 22062 #checksum 2404

Db  2; Score 1050; Match 81.9%; QryMatch 85.9%; Pred. No. 8.45e-151;
Matches 136; Conservative 19; Mismatches 10; Indels 1; Gaps 1;

Db  24 cmlsqthlnrtrtlmalnagmrissfscldkrdhdfpqqefdgngfqkaaisvlhem 83
      |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  1 CDLPQTHSIGSRRTMLLAQMRRISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  84 mqqtfnlfsknsaaawdetllkfyielfqmndleacvigeqvgeetplmmedsilav 143
      |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  60 IQQIFNLFSKDSAAWDETLLDKFYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  144 kkyfqrtilylekkykspcawevvraeimsrfsfsltnlqeslrskd 189
      :||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  120 RKYFQRITLYLKEKYSKPCAWEVVRAEIMRSFSLTNLQESLSRKE 165

RESULT 4
ENTRY   D25843
TITLE   interferon alpha-G - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM #formal name Homo sapiens #common name man
DATE     16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
         27-Jan-1995
ACCESSIONS D25843
REFERENCE  A91374
#authors   Ohara, O.; Teraoka, H.
#journal   FEBS Lett. (1987) 211:78-82
#title     Anomalous behavior of human leukocyte interferon subtypes on
           polyacrylamide gel electrophoresis in the presence of
           dodecyl sulfate.
#cross-references MUID:87105954
#accession D25843
#molecule_type mRNA
#residues  1-167 ##label OHA
#note      sequence not compared to nucleotide translation
           nucleotide sequence is not given
CLASSIFICATION #superfamily interferon alpha
SUMMARY       #length 167 #molecular-weight 19540 #checksum 57

```

```

Db  4; Score 1050; Match 84.9%; QryMatch 85.9%; Pred. No. 8.45e-151;
Matches 141; Conservative 14; Mismatches 10; Indels 1; Gaps 1;

Db  2 cdllpqtshlnrtrtlmalnagmrissfscldkrdhdfpqqefdgngfqkaaisvlhem 61
      |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  1 CDLPQTHSIGSRRTMLLAQMRRISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  62 iqqtfnlfskdsaaadetlldkfyelyqqindleacmmdegvgvedtplmndvsiltv 121
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  60 IQQIFNLFSKDSAAWDETLLDKFYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  122 rkyfqrtilylekkykspcawevvraeimsrfsfsltnlqeslrskd 167
      ||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  120 RKYFQRITLYLKEKYSKPCAWEVVRAEIMRSFSLTNLQESLSRKE 165

RESULT 5
ENTRY   IVHU16
TITLE   interferon alpha-I-6 precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-6; LeIF K; type I interferon
ORGANISM #formal name Homo sapiens #common name man
DATE     28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
         18-Nov-1994
ACCESSIONS A23753
REFERENCE  A92916
#authors   Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
           J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
           Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
           Weissmann, C.
#journal   J. Mol. Biol. (1985) 185:227-260
#title     Structural relationship of human interferon alpha genes and
           pseudogenes.
#cross-references MUID:86037205
#accession A23753
#molecule_type DNA
#residues  1-189 ##label HEN
GENETICS
#gene      IFNA
#map_position 9p22-p13
CLASSIFICATION #superfamily interferon alpha
KEYWORDS      antiviral
FEATURE
  1-23        #domain signal sequence #status predicted #label SIG\
  24-189      #product interferon alpha-I-6 #label MAT\
  24-122,52-162 #disulfide bonds #status predicted
SUMMARY       #length 189 #molecular-weight 22140 #checksum 4413

Db  2; Score 1049; Match 86.1%; QryMatch 85.8%; Pred. No. 1.25e-150;
Matches 143; Conservative 8; Mismatches 14; Indels 1; Gaps 1;

Db  24 cdllpqtshlghrrtmllaqmrrislfscldkrdhdfpqqefdgngfqkaaisvlhev 83
      |:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  1 CDLPQTHSIGSRRTMLLAQMRRISLFCIKDRDRFGFPQEEF-GNQFQKAETIPVLHEM 59
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  84 iqqtfnlfskdsaaawderlldkfyelyqqindleacmvewvggtplmmedsilav 143
      |||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  60 IQQIFNLFSKDSAAWDETLLDKFYELYQQINDLEACVIGVGVTETPLMKEDSILAV 119
      :|||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

Db  144 rkyfqrtilylekkykspcawevvraeimsrfsfsltnlqeslrskd 189
      ||||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Qy  120 RKYFQRITLYLKEKYSKPCAWEVVRAEIMRSFSLTNLQESLSRKE 165

RESULT 6

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Db 122 kkyfqrityllytekkyspcawevvraeimsrfsfslkfqrirkte 167
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRFSLSLTNIQESLSRKE 165

RESULT 9
ENTRY A22255 #type complete
TITLE Interferon alpha-I' precursor - human
ORGANISM #formal name Homo sapiens #common name man
DATE 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change
18-Jun-1993
ACCESSIONS A22255
REFERENCE A22255
#authors Mizoguchi, J.; Pitha, P.M.; Raj, N.B.K.
#journal DNA (1985) 4:221-232
#title Efficient expression in Escherichia coli of two species of
human interferon-alpha and their hybrid molecules.
#cross-references M01D:85229953
#accession A22255
#molecule_type mRNA
#residues 1-189 ##label M1Z
CLASSIFICATION #superfamily interferon alpha
FEATURE
24-189 #product interferon-alpha-I' #label MAT
SUMMARY #length 189 #molecular-weight 21728 #checksum 2510

Db 4; Score 1026; Match 81.3%; QryMatch 84.0%; Pred. No. 9.26e-147;
Matches 135; Conservative 19; Mismatches 11; Indels 1; Gaps 1;

Db 24 cdlpqthslgnrralllaqmgrishfscldkrdhfglpqefdnqfqtqaisvlhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRIISLFSCLKDRDRFCFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstksaawdetlldkfyielfqqlndleacvtqevgveeialmmedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLLDKFYELYQQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrityllytekkyspcawevvraeimsrfsfsltnqlkrlrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRFSLSLTNIQESLSRKE 165

RESULT 10
ENTRY IVHU16 #type complete
TITLE Interferon alpha-I-16 precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-16; type I interferon
ORGANISM #formal name Homo sapiens #common name man
DATE 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
18-Nov-1994
ACCESSIONS G23753
REFERENCE A29216
#authors Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
Weismann, C.
#journal J. Mol. Biol. (1985) 185:227-260
#title Structural relationship of human interferon alpha genes and
pseudogenes.
#cross-references M01D:86037205
#accession G23753
#molecule_type DNA
#residues 1-189 ##label HEN
GENETICS IFNA
#gene

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#map_position 9p22-p13
CLASSIFICATION #superfamily interferon alpha
KEYWORDS antiviral
FEATURE
1-23 #domain signal sequence #status predicted #label SIG
24-189 #product interferon alpha-I-16 #label MAT
24-122,52-162 #disulfide bonds #status predicted
SUMMARY #length 189 #molecular-weight 21711 #checksum 45

Db 2; Score 1025; Match 82.5%; QryMatch 83.9%; Pred. No. 1.36e-146;
Matches 137; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Db 24 cdlpqthslgnrralllaqmgrishfscldkrdyfgfpqevfdngfqkqaisafhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRIISLFSCLKDRDRFCFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstksaawdetlldkfyielfqqlndleacvtqevgveeialmmedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLLDKFYELYQQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrityllytekkyspcawevvraeimsrfsfsltnqlkrlrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRFSLSLTNIQESLSRKE 165

RESULT 11
ENTRY A22068 #type complete
TITLE Interferon alpha-I-Wa - human
ORGANISM #formal name Homo sapiens #common name man
DATE 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change
30-Sep-1993
ACCESSIONS A22068
REFERENCE A22068
#authors Torczynski, R.M.; Fuke, M.; Bollon, A.P.
#journal Proc. Natl. Acad. Sci. U.S.A. (1984) 81:6451-6455
#title Human genomic library screened with 17-base oligonucleotide
probes yields a novel interferon gene.
#cross-references M01D:85038533
#accession A22068
#status preliminary
#molecule_type DNA
#residues 1-189 ##label TOR
CLASSIFICATION #superfamily interferon alpha
SUMMARY #length 189 #molecular-weight 21711 #checksum 45

Db 4; Score 1025; Match 82.5%; QryMatch 83.9%; Pred. No. 1.36e-146;
Matches 137; Conservative 14; Mismatches 14; Indels 1; Gaps 1;

Db 24 cdlpqthslgnrralllaqmgrishfscldkrdyfgfpqevfdngfqkqaisafhem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRIISLFSCLKDRDRFCFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstksaawdetlldkfyielfqqlndleacvtqevgveeialmmedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQIFNLFSTKDSAAWDETLLDKFYELYQQQLNDLEACVIGVGVTETPLMKEDSILAV 119

Db 144 rkyfqrityllytekkyspcawevvraeimsrfsfsltnqlkrlrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVWRAEIMRFSLSLTNIQESLSRKE 165

RESULT 12
ENTRY IVHU09 #type complete
TITLE Interferon alpha-9 precursor - human

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ORGANISM      #formal_name Homo sapiens #common_name man
DATE          01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
              30-Sep-1993
ACCESSIONS    A01835
REFERENCE      A94255
#authors      Lawn, R.M.; Adelman, J.; Dull, T.J.; Gross, M.; Goeddel, D.;
              Ullrich, A.
#journal      Science (1981) 212:1159-1162
#title        DNA sequence of two closely linked human leukocyte interferon
              genes.
#cross-references M01D:81201124
#accession    A01835
#molecule_type DNA
#residues     1-189 ##label LAW
#note         residues 1-23 correspond to the signal sequence
CLASSIFICATION #superfamily interferon alpha
SUMMARY       #length 189 #molecular-weight 21688 #checksum 2966

Db 2; Score 1023; Match 81.3%; QryMatch 83.7%; Pred. No. 2.96e-146;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdtpqthslgnrralllqgmgrispfscldkrdpfglpqeeefdqngfktqaisvlihem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFSCLKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstedsaaaweqsllkfstelyqqlnleacvigeqvmeetplmmedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQTFNLFSSTKDSAAWDETLLDKFYELYQQLNLEACVIGQGVGTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsrfsfstnlqlrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 13
ENTRY        IVH0A5      #type complete
TITLE        interferon alpha-5 precursor - human
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         01-Sep-1981 #sequence_revision 01-Sep-1981 #text_change
              18-Nov-1994
ACCESSIONS   A60937; A01830
REFERENCE     A60937
#authors      Bartholomew, C.; Windass, J.D.
#journal      J. Interferon Res. (1989) 9:407-417
#title        Identification of a functional allele of a human
              interferon-alpha gene previously characterized as a
              pseudogene.
#accession    A60937
#molecule_type DNA
#residues     1-189 ##label BAR
#note         this genomic sequence, SWTIII.1A, encodes a functional
              allele for alpha interferon at the locus pseudo-leIF-L
              that, in other allelic forms, contains a stop codon at
              the end of the signal sequence and is a pseudogene

REFERENCE     A93249
#authors      Goeddel, D.V.; Leung, D.W.; Dull, T.J.; Gross, M.; Lawn,
              R.M.; McCandless, R.; Seeburg, P.H.; Ullrich, A.;
              Yelverton, E.; Gray, P.W.
#journal      Nature (1981) 290:20-26
#title        The structure of eight distinct cloned human leukocyte
              interferon cDNAs.
#cross-references M01D:81148795
#accession    A01830
#molecule_type mRNA

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#residues     1-189 ##label GOE
#note         eight classes of interferon alpha clones were
              identified; this sequence is derived from class C
CLASSIFICATION #superfamily interferon alpha
FEATURE       1-23
SUMMARY       #domain signal sequence #status predicted #label SIG
              #length 189 #molecular-weight 21835 #checksum 2522

Db 2; Score 1017; Match 81.3%; QryMatch 83.2%; Pred. No. 3.03e-145;
Matches 135; Conservative 18; Mismatches 12; Indels 1; Gaps 1;

Db 24 cdtpqthslgnrralllqgmgrispfscldkrdhfrfpqeeefdqngfktqaisvlihem 83
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFSCLKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 84 iqqtfnlfstedsaaaweqsllkfstelyqqlnleacvigeqvmeetplmmedsilav 143
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQTFNLFSSTKDSAAWDETLLDKFYELYQQLNLEACVIGQGVGTETPLMKEDSILAV 119

Db 144 rkyfqrtilytkkyspcawevvraeimsrfsfstnlqlrrkd 189
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 14
ENTRY        F25843      #type complete
TITLE        interferon alpha-J - human
ALTERNATE_NAMES human leukocyte interferon (IFN)
ORGANISM     #formal_name Homo sapiens #common_name man
DATE         16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change
              27-Jan-1995
ACCESSIONS   F25843
REFERENCE     A91374
#authors      Ohara, O.; Teraoka, H.
#journal      FEBS Lett. (1987) 211:78-82
#title        Anomalous behavior of human leukocyte interferon subtypes on
              polyacrylamide gel electrophoresis in the presence of
              dodecyl sulfate.
#cross-references M01D:87105954
#accession    F25843
#molecule_type mRNA
#residues     1-167 ##label OHA
#note         sequence not compared to nucleotide translation
              nucleotide sequence is not given
#note         #superfamily interferon alpha
CLASSIFICATION #superfamily interferon alpha
SUMMARY       #length 167 #molecular-weight 19737 #checksum 451

Db 4; Score 1012; Match 79.5%; QryMatch 82.8%; Pred. No. 2.10e-144;
Matches 132; Conservative 20; Mismatches 13; Indels 1; Gaps 1;

Db 2 cdtpqthslgnrralllqgmgrispfscldkrdhfrfpqeeefdqngfktqaisvlihem 61
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 1 CDLPQTHSLGSRRTMLLAQMRRISLFSCLKDRDRDFGFPQEEF-GNQFQKAETIPVLHEM 59

Db 62 iqqtfnlfstedsaaaweqsllkfstelyqqlnleacvigeqvmeetplmmedfilav 121
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 60 IQQTFNLFSSTKDSAAWDETLLDKFYELYQQLNLEACVIGQGVGTETPLMKEDSILAV 119

Db 122 rkyfqrtilytkkyspcawevvraeimsrfsfstnlqlrrkd 167
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Qy 120 RKYFQRITLYLKEKKYSPCAWEVRAEIMRSFSLSTNLQESLSRKE 165

RESULT 15

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Aug 29 16:53

/home/pandya/smith249671/US-08-249-671-5.rpr

13

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ENTRY          IVRU18      #type complete
TITLE          interferon alpha-I-8 precursor - human
ALTERNATE_NAMES HuIFN-alpha-I-8; type I interferon
ORGANISM       Homo sapiens #common name man
DATE           28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change
              18-Nov-1994
ACCESSIONS     D23753
REFERENCE      A92916
AUTHORS        Henco, K.; Brosius, J.; Fujisawa, A.; Fujisawa, J.I.; Haynes,
              J.R.; Hochstadt, J.; Kovacic, T.; Pasek, M.; Schambeck, A.;
              Schmid, J.; Todokoro, K.; Walchli, M.; Nagata, S.;
              Weissmann, C.
JOURNAL        J. Mol. Biol. (1985) 185:227-260
TITLE          Structural relationship of human interferon alpha genes and
              pseudogenes.
CROSS-REFERENCES MUID:86037205
ACCESSION      D23753
MOLECULE_TYPE  DNA
RESIDUES       1-189 ##label HEN
GENETICS
GENE           IFNA
MAP_POSITION   9p22-pl3
CLASSIFICATION #superfamily interferon alpha
KEYWORDS       antiviral
FEATURE
1-23          #domain signal sequence #status predicted #label SIG\
24-189        #product interferon alpha-I-8 #label MAT\
24-122,52-162 #disulfide bonds #status predicted
SUMMARY       #length 189 #molecular-weight 21989 #checksum 1052

DB 2; Score 1012; Match 82.5%; QryMatch 82.8%; Pred. No. 2.10e-144;
Matches 137; Conservative 13; Mismatches 15; Indels 1; Gaps 1;

Db 24 cdlpqtshlgnrralillagarrispclskdrhdfpqaefddkfgkagaisvlhem 83
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 1 CDLPQTHSLGSRRTMLLAQMRRISLFSCLKDRDRDFGPQEEFGN-QFQAEIPIVLHEM 59

Db 84 iqqtfnlfstkdssaalddetilldefyielddqldndlescvmqevqviesplmyedsilav 143
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 60 IQQIFNLFSTKSSAAWDETLDDKFTELYQQLDLEACVIGGVGVTTPLMKEDSILAV 119

Db 144 rkyfqrtilylekkysscawevvraeimrfsislndqrlrkeke 189
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY 120 RKYFQRITLYLKEKYSKPCAEVVRAEIMRFSISLTNLQESLRSKE 165

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Search completed: Tue Aug 29 17:05:11 1995
Job time : 23 secs.

PT O-glycosylated alpha-interferon - used for treatment of
 PT viral of tumour diseases
 PS Disclosure; Fig 6(A+B); 104pp; English.
 CC Plasmid pAD-CMV19 (6.1 kb) is incubated with HindIII and XbaI, then
 CC ligated with a modified cDNA fragment for human IFN-alpha2c. This
 CC fragment is obtd. from the known clone IF7 by PCR-modification of
 CC the 5'-noncoding region to replace it with the corresp. region from
 CC human beta-globulin mRNA. This modification significantly improves
 CC expression by increasing the efficiency of initiation of translation.
 CC The recombinant prod. is designated pAD19b-IFN.
 CC See also Q20731-43 and Q20522-26.
 SQ Sequence 639 BP; 171 A; 155 C; 152 G; 161 T;

DB 3; Score 495; Match 100.0%; QryMatch 100.0%; Pred. No. 5.68e-311;
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 126 tgtgatcgtcctcaaacccacagcctggtagcaggaggaacttgatcctcgtgacag 185
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 TGTGATCTGCTCAAAACCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 186 atgaggagaatctctttctcgttgaagcagacagcgtgacttgattgattccccag 245
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGGACAGACGTGACTTTGGATTTCCCCAG 120

Db 246 gagagtttggaacccagttccaaaaggctgaacacatcctctcctccatgagatgate 305
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 121 GAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAACCCATCCCTGTCTCCATGAGATGATC 180

Db 306 cagcagatcttcaatctcttcagcacaaggaactcatcgtgcttggtgagaccctc 365
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 181 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGATGAGACCCCTC 240

Db 366 ctagacaattctacactgaactctaccagcagctgaatgaactggaactgtgtgata 425
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 241 CTAGACAATTTCTACACTGAATCTTACCAGCAGCTGATGACCTTGAAGCCTGTGTGATA 300

Db 426 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 485
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 301 CAGGGGGTGGGGGTGACAGACTCCCTTGATGAAGGAGGACTCCATTTGGCTGTGAGG 360

Db 486 aaatcttccaaagaatacactctctatctgaagagaagaatacagccctgtgctagg 545
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 361 AAATACTTCCAAAGAATCACTCTATCTGAAAGAGAAATACAGCCCTTTGCTGCTGG 420

Db 546 gaggtgtcagcagagaataatcagatctttttctttgtcaacaacttgcagaagaagt 605
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 421 GAGGTTGTGACAGCAGAAATCATGAGATCTTTTCTTGTCAACAACCTTGCAAGAAAGT 480

Db 606 ttaagaagtaaggaa 620
 ||||||||||||||||
 Qy 481 TTAAGAATAGGAA 495

RESULT 2
 ID N70528 standard; DNA; 501 BP.
 AC N70528;
 DT 20-MAY-1991 (first entry)
 DE Sequence encoding IFN-alpha-2 (Arg).
 KW Hybrid alpha/omega interferon; antiviral; virucide; antitumour;
 KW cytostatic; ss.
 FH Key Location/Qualifiers
 FT CDS 1..501
 FT /*tag= a
 PN EP-236920-A.

PD 16-SEP-1987.
 PF 04-MAR-1987; 103030.
 PR 10-MAR-1986; DE-607835.
 PA (BOEH) BOEHRINGER INGELHEIM.
 PI Hauptmann R, Swetly P, Meindl P, Gunther A, Falkner E,
 PI Bodo G, Maurer-Fogy I;
 WPI; 87-258223/37.
 DR P-PSDB; P70329.

PT New hybrid interferon prods. useful as antiviral agents - contg.

PT alpha and omega interferon fragments
 PS Disclosure; pp4-6; 65pp; German.
 CC Hybrid interferons comprising a fragment of an alpha-interferon and
 CC a fragment of an omega-interferon, and their N-terminal Met or
 CC N-formyl-Met derivs. and N-glycosylated derivs., are new. The hybrid
 CC interferons are useful as antiviral and antitumour agents. Both IFN-
 CC alpha-2(Arg) and omega-1-interferon has a 191-196 BgIII restriction
 CC site (see N70528 and N70529). In addition, IFN-alpha-2(Arg) has a
 CC 451-456 BgIII site.
 SQ Sequence 501 BP; 141 A; 116 C; 123 G; 121 T;

DB 2; Score 495; Match 100.0%; QryMatch 100.0%; Pred. No. 5.68e-311;
 Matches 495; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 4 tgtgatcgtcctcaaacccacagcctggtagcaggaggaacttgatcctcgtgacag 63
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 1 TGTGATCTGCTCAAAACCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 64 atgaggagaatctctctttctcgttgaagcagacagcgtgacttgattgattccccag 123
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 61 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGGACAGACGTGACTTTGGATTTCCCCAG 120

Db 124 gaggaatttggaacccagttccaaaaggctgaacacatcctctcctccatgagatgate 183
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 121 GAGGAGTTTGGCAACAGCTTCCAAAAGGCTGAACCCATCCCTGTCTCCATGAGATGATC 180

Db 184 cagcagatcttcaatctcttcagcacaaggaactcatcgtgcttggtgagaccctc 243
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 181 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGATGAGACCCCTC 240

Db 244 ctagacaattctacactgaactctaccagcagctgaatgaactggaactgtgtgata 303
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 241 CTAGACAATTTCTACACTGAATCTTACCAGCAGCTGATGACCTTGAAGCCTGTGTGATA 300

Db 304 cagggggtgggggtgacagagactccctgatgaaggaggactccattctggctgtgagg 363
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 301 CAGGGGGTGGGGGTGACAGACTCCCTTGATGAAGGAGGACTCCATTTGGCTGTGAGG 360

Db 364 aaatacttccaaagaatacactctctatctgaagagaagaatacagccctgtgctagg 423
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 361 AAATACTTCCAAAGAATCACTCTATCTGAAAGAGAAATACAGCCCTTTGCTGCTGG 420

Db 424 gaggtgtcagcagagaataatcagatctttttctttgtcaacaacttgcagaagaagt 483
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Qy 421 GAGGTTGTGACAGCAGAAATCATGAGATCTTTTCTTGTCAACAACCTTGCAAGAAAGT 480

Db 484 ttaagaagtaaggaa 498
 ||||||||||||||||
 Qy 481 TTAAGAATAGGAA 495

RESULT 3
 ID Q20764 standard; DNA; 639 BP.
 AC Q20764;
 DT 21-APR-1992 (first entry)

CC crossover region common to both sequences. The hybrid sequences are
CC obtd. without the need for chance availability of restriction sites
CC to be combined. Sequential deletions to give prods. with modified
CC properties, activity and specificity are reliable.
SQ Sequence 589 BP; 165 A; 135 C; 135 G; 154 T;

DB 3; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 1.31e-309;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 1 tgtgatctgctcaaacccacagctgggtagcagagagacattgatctctctggcacag 60
Qy 1 TGTGATCTGGCTCAAAACCCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 61 atgaggagaatctctctttctctgcttgaagacagacatgacttggatttccccag 120
Qy 61 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGCAGACAGCTGACTTTGGATTTCCCCAG 120

Db 121 gaggggttggaacacagcttccaaaaggctgaacaccatccctgtcctccatgagatgac 180
Qy 121 GAGGAGTTGGCAACAGTTCCAAAAGGCTGAACCATCCCTGTCTCCATGACATGATC 180

Db 181 cagcagatcttcaatctctcagcaaaaggactcaatctgcttgggatgagaccctc 240
Qy 181 CAGCAGATCTTCAATCTCTCAGCAAAAGGACTCATCTGCTGCTTGGGATGAGCCCTC 240

Db 241 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 300
Qy 241 CTAGACAAATTTCTACACTGAACCTTACCAGCAGCTGAATGACCTGGAGCCTGTGTGATA 300

Db 301 caggggttggggtgacagagactccctgatgagagaggactccattctggtgtgagg 360
Qy 301 CAGGGGTGGGGGTGACAGACTCCCTGTGATGAGGAGGACTCCATTCTGGCTGTGAGG 360

Db 420 aaatacttccaaagaatcaactctctatctgaagagaagaataacagcccttgtgctgg 420
Qy 420 AAATACTTCCAAAGAATCACTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 420

Db 480 gaggtgtcagagcagaataatcagatcttttttttttttttttttttttttttttttttt 480
Qy 421 GAGGTTGTGAGCAGCAAAATCATGAGATCTTTTCTTTTCTCACAAACTTGCAGAAAGT 480

Db 481 ttaagaagtaaggaa 495
Qy 481 TTAAGAGTAAGGAA 495

RESULT 5
ID N60399 standard; DNA; 1863 BP.
AC N60399;
DT 25-JUN-1991 (first entry)
DE Sequence of the promoter region 22 of the alcA gene, the synthetic
DE signal peptide coding region 68 and the coding region 60 coding for
DE human interferon alpha-2 in pALCALISFN.
KW Filamentous fungi promoter; ds.
FH Key Location/Qualifiers
FT misc feature 29
FT /*tag= a
FT /note= * = base 1200*
FT sig_peptide 878..922
FT /*tag= b
FT CDS 923..975
FT /*tag= c
FT mat_peptide 976..1474
FT /*tag= d

PN W08606097-A.
PD 23-OCT-1986.
PF 14-APR-1986; G00209.
PR 15-APR-1985; CA-479135.
PR 20-DEC-1985; US-811404.
PA (ALIE-) ALIELIX INC.
PI Gwynne DI, Buxton F, Pickett M, Davies R, Scazzocchio C;
DR WPI; 86-291664/44.
PT DNA construct for use in filamentous fungi - comprising promoter
PT operative in filamentous fungi to promote transcription of coding
PT region
PS Disclosure; Fig 11; 75pp; English.
CC In the constructs of the invention, the promoter region naturally
CC associated with the alcohol dehydrogenase I (alcA) gene and the
CC aldehyde dehydrogenase (aldA) gene of A. nidulans or naturally
CC associated with the glucoamylase gene in Aspergillus niger may be
CC used. The DNA construct may contain a promoter region in operative
CC association with a signal peptide coding region. The promoter/signal
CC construct is suitably provided with a flanking restriction site to
CC allow precise coupling of the protein coding region to the signal
CC peptide coding region.
SQ Sequence 1863 BP; 516 A; 425 C; 422 G; 500 T;

DB 2; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 1.31e-309;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 977 tgtgatctgctcaaacccacagctgggtagcagagagacattgatctctctggcacag 1036
Qy 1 TGTGATCTGGCTCAAAACCCACAGCCTGGGTAGCAGGAGGACCTTGATGCTCTGGCACAG 60

Db 1037 atgaggagaatctctctttctctgcttgaagacagacatgacttggatttccccag 1096
Qy 61 ATGAGGAGATCTCTCTTTCTCTGCTTGAAGCAGACAGCTGACTTTGGATTTCCCCAG 120

Db 1097 gaggggttggaacacagcttccaaaaggctgaacaccatccctgtcctccatgagatgac 1156
Qy 121 GAGGAGTTGGCAACAGTTCCAAAAGGCTGAACCATCCCTGTCTCCATGAGATGATC 180

Db 1157 cagcagatcttcaatctctcagcaaaaggactcaatctgcttgggatgagaccctc 1216
Qy 181 CAGCAGATCTTCAATCTCTTTCAGCAAAAGGACTCATCTGCTTGGGATGAGCCCTC 240

Db 1217 ctagacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 1276
Qy 241 CTAGACAAATTTCTACACTGAACCTTACCAGCAGCTGAATGACCTTGCAGCCCTGTGTGATA 300

Db 1277 caggggttggggtgacagagactccctgatgagagaggactccattctggtgtgagg 1336
Qy 301 CAGGGGTGGGGGTGACAGACTCCCTGTGATGAGGAGGACTCCATTCTGGCTGTGAGG 360

Db 1337 aaatacttccaaagaatcaactctctatctgaagagaagaataacagcccttgtgctgg 1396
Qy 361 AAATACTTCCAAAGAATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 420

Db 1397 gaggtgtcagagcagaataatcagatcttttttttttttttttttttttttttttttttt 1456
Qy 421 GAGGTTGTGAGCAGCAAAATCATGAGATCTTTTCTTTTCTCACAAACTTGCAGAAAGT 480

Db 1457 ttaagaagtaaggaa 1471
Qy 481 TTAAGAGTAAGGAA 495

RESULT 6

ID N10011 standard; DNA; 744 BP.
AC N10011;
DT 13-AUG-1992 (first entry)
DE Sequence of the Hif-II-206 fragment of culture HcIF-G encoding
DE interferon (IFN) -alpha-2 and signal sequence.
KW Anti-viral agent; anti-cancer agent; therapy; tumour; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT sig_peptide 2..52
FT /*tag= a
FT mat_peptide 53..550
FT /*tag= b
PN EP--32134-A.
PD 15-JUL-1981.
PF 07-JAN-1981; 300050.
PR 08-JAN-1980; EP-300079.
PR 03-APR-1980; EP-301100.
PR 02-OCT-1980; GB-031737.
PA (BIOJ) BIOGEN NV.
PI Weissmann C;
DR WPI; 81-53697D/30.
DR P-PSDB; P10018.
PT DNA sequences coding for interferon-like polypeptide(s) - useful
PT as antiviral or antitumour agents
PS Claim 6; Fig 12-16; 136pp; English.
CC The inventors claim DNA sequences coding for interferon-like
CC polypeptide(s). The DNA sequences pref. encode IFN-alpha type 1, 2,
CC 4a and 4b. Pref. DNA sequences which hybridise to the inserts of Z-
CC pBR322(pst)/HcIF-4c, Z-pBR322(pst)/HcIF-2h, Z-pBR322(pst)/HcIF-SN35,
CC Z-pBR322(pst)/HcIF-SN42 and ZpK287(pst)/HcIF-2h-AH6 comprise
CC Z-pBR322(pst)/HcIF-II-206, Z-pBR322(pst)/HcIF-SN35-AHL6, and
CC Hif-chr1, -3, -12, -13, -16, -26, -30, -35, -19 and -27. Pref.
CC recombinant DNA molecules are C8-IFN-alpha-1, C8-IFN-alpha-2,
CC LAC-AUG(alpha-2) and beta-lac-AUG(alpha-2). A comparison of the
CC nucleotide sequence of the coding region of HcIF-35NB-alpha and
CC that of Hif-2h (coding region) reveals that they are identical.
SQ Sequence 744 BP; 202 A; 171 C; 169 G; 202 T;

DB 4; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 1.31e-309;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 53 tgtgatctgctcaaacccacagctgggtgagcaggagacattgatgctctggccag 112
|||||
Qy 1 TGTGATCTGCTCAAAACCCACAGCTGGGTAGCAGGAGGACCTTGATGCTCTGGCAG 60

Db 113 atgaggagaatctctcttctctctgttgaagcagacagacatgattgattccccag 172
|||||
Qy 61 ATCAGGAGATCT 120

Db 173 gaggagttggcaacagcttccaaaaggctgaaccatccctgtcctccatgagatgac 232
|||||
Qy 121 GAGGAGTTGGCAACAGCTTCAAAAAGGCTGAACCATCCCTGTCTCTCCATGAGATGATC 180

Db 233 cagcagattctcaattctctcagcaaaaggactcaatcgtctggtgagatgagaccctc 292
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTGCTGGATGAGACCTC 240

Db 293 ctagacaaattctacactgaactctaccagcagctgaatgacctggaacctgtgtgata 352
|||||
Qy 241 CTAGCAAAATTTACACTGAATCTTACAGCAGCTGAATGACCTTGGAGCCTGTGTGATA 300

Db 353 caggggggtgggggtgacagagactccctgatgaaggaggactccattctggtgtgagg 412
|||||
Qy 301 CAGGGGGTGGGGGTGACAGACTCTCCCTGATGAAGGAGGACTCCATTGTGCTGTGAGG 360

Db 413 aaatacttcaagaatcactctctatctgaaagaagaataacagcccttgctgctg 472
|||||
Qy 361 AATATCTTCCAGATCACTCTCTATCTGAAAGAGAGAAATACAGCCCTTGTGCTGG 420

Db 473 gaggttgctcagacagaaatcatgagatcttttcttcttcaacaaacttcaagaagt 532
|||||
Qy 421 GAGGTTGTCAGACAGAAATCATCATCTTTCTTTCTGTAACAACACTTCAAGAAAT 480

Db 533 ttaagaagtaaggaa 547
|||||
Qy 481 TTAAGAAGTAAGGAA 495

RESULT 7
ID Q47153 standard; cDNA; 647 BP.
AC Q47153;
DT 21-JAN-1994 (first entry)
DE Natural human interferon-alpha cDNA.
KW IFN-alpha; hIFN-alpha; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 1..504
FT /*tag= a
PN EP-553494-A.
PD 04-AUG-1993.
PF 29-DEC-1992; 122084.
PR 31-DEC-1991; KR-025878.
PR 31-DEC-1991; KR-025879.
PR 28-JAN-1992; KR-001155.
PA (LUCK-) LUCKY LTD.
PI Bae TO, Chang HJ, Cho JM, Park SJ, Park YW.
DR WPI; 93-244548/31.
DR P-PSDB; R38793.
PT Recombinant human alpha interferon and corresp. gene - for
PT efficient expression in yeast, and purificn. process
PS Disclosure; Fig 1B; 30pp; English.
CC The sequence is that of natural human interferon-alpha cDNA.
SQ Sequence 647 BP; 174 A; 154 C; 151 G; 168 T;

DB 7; Score 491; Match 99.6%; QryMatch 99.2%; Pred. No. 3.03e-308;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 76 tgtgatctgctcaaacccacagctgggtgagcaggagacattgatgctctggccag 135
|||||
Qy 1 TGTGATCTGCTCAAAACCCACAGCTGGGTAGCAGGAGGACCTTGATGCTCTGGCAG 60

Db 136 atgaggaaatctctcttctctctgcttgaaggacagacatgactttggatttccccag 195
|||||
Qy 61 ATCAGGAGATCT 120

Db 196 gaggagttggcaaccagttccaaaaggctgaaccatccctgtcctccatgagatgac 255
|||||
Qy 121 CAGGAGTTGGCAACAGCTTCCAAAAGGCTGAACCATCCCTGTCTCTCCATGAGATC 180

Db 256 cagcagattctcaattctctcagcacaaggactcatctgctgcttgggatgagaccctc 315
|||||
Qy 181 CAGCAGATCTTCAATCTCTTCAGCAAAAGGACTCATCTGCTGCTGGATGAGACCTC 240

Db 316 ctagacaaattctacactgaactctaccagcagctgaatgacctggaacctgtgtgata 375
|||||
Qy 241 CTAGCAAAATTTACACTGAATCTTACAGCAGCTGAATGACCTTGGAGCCTGTGTGATA 300

Db 376 caggggggtgggggtgacagagactccctgatgaaggaggactccattctggtgtgagg 435

- QY 301 CAGGGGTGGGGTGACAGACTCCCTGATGAAGGAGACTCCATTCTGGCTCTCAGG 360
|||||
Db 436 aaatacttccaaagaatcaactctctatctgaagaagaagaataacagccctgtgctgg 495
|||||
QY 361 AATACTTCCAAAGAATCACTCTCTATCTGAAGACAGAGAAATACAGCCCTGTGGCTGG 420
|||||
Db 496 gaggtgtcagagcagaagaatcatgagatcttttttgcacaacaacttgcaagaagt 555
|||||
QY 421 GAGTTGTCTGACAGCAGAAATCATGATCTTTTCTTCTCAACAACTTGCAGAAAGT 480
|||||
Db 556 ttaagaagtaaggaa 570
|||||
QY 481 TTAAGAAGTAAGGAA 495
|||||

RESULT 8.

ID N20090 standard; cDNA; 958 BP.
AC N20090;
DT 10-AUG-1992 (first entry)
DE Sequence of leukocyte interferon LeIF A cDNA.
KW Viral infection; therapy; malignancy; ss.
OS Homo sapiens.
FH Key Location/Qualifiers
FT CDS 60..626
FT /tag= a
PN GB2079291-A.
PD 20-JAN-1982.
PF 01-JUL-1981; 120279.
PR 01-JUL-1980; US-164986.
PR 08-SEP-1980; US-184909.
PR 10-NOV-1980; US-205578.
PR 21-APR-1981; US-256204.
PA (HOFF) HOFFMANN-LA ROCHE AG.
PA (GENE-) GENENTECH INC.
PI Goeddel DYN, Pestka S;
DR WPI; 82-04460E/03.
DR P-PSDB; P20103.
PT Mature human leukocyte interferon polypeptide(s) - prepd. from
PT microbes transformed with appropriate DNA sequences
PS Claim 34; Fig 3; 20pp; English.
CC The inventors claim a polypeptide comprising the AA sequence of a
CC mature human LeIF and a DNA sequence encoding it. LeIF A-D, F, H-J
CC and encoding DNA are specifically claimed. They are natural allelic
CC variations. LeIF is isolated from the leukocytes of humans with
CC chronic myelogenous leukaemia, induced to produce interferon with
CC Sendai or Newcastle disease virus; esp. the cell line KG-1.
SQ Sequence 958 BP; 266 A; 211 C; 193 G; 288 T;

DB 4; Score 491; Match 99.6%; OryMatch 99.2%; Pred. No. 3.03e-308;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 130 tgtgatctgcttcaaacaccagcctgggtagcagagagaccttgatgctctggcacag 189
|||||
QY 1 TGTGATCTGGCTCAAAACCCAGCCCTGGGTAGCAGGAGGACTTGTGCTCGGCACAG 60
|||||
Db 190 atgaggaataatctcttttctctgttgatgaaggacagacatgaattgttcccccag 249
|||||
QY 61 ATCAGCAGAAATCTCTTTTCTCTCTCTGAAGGACACACGCTGACTTTTCCCCAG 120
|||||
Db 250 gagggagttggcaacagttccaaaaggctgaaacaccatccctgtctctcatgagatgc 309
|||||
QY 121 GAGGAGTTTGGCAACCACTTCCAAAGGCTGAACCATCCCTGTCTCCATCATGATGATC 180
|||||

Db 310 cagcagatcttcaatctctcagcacaaaggactcatctgtctgttggatgagacctc 369
|||||
QY 181 CAGCAGATCTTCAATCTCTTCAGCACAAAGGACTCATCTGTCTTGGGATCAGACCCTC 240
|||||
Db 370 ctgacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
|||||
QY 241 CTAGACAAATTTACACTGAACCTTACAGCAGCTGAATGACCTTGGAAAGCCTGTGTGATA 300
|||||
Db 430 cagggggtgggggtgacagagactccctgatgaaggagagactccattctggctgtgagg 489
|||||
QY 301 CAGGGGTGGGGGTGACAGACTCCCTGATGAAGGAGACTCCATTCTGGCTGTGAGG 360
|||||
Db 490 aaatacttccaaagaatcaactctctatctgaagaagaagaataacagccctgtgctgg 549
|||||
QY 361 AATACTTCCAAAGAATCATCTCTATCTGAAGACAGAGAAATACAGCCCTTGTGCTGG 420
|||||
Db 550 gaggtgtcagagcagaagaatcatgagatcttttttgcacaacaacttgcaagaagt 609
|||||
QY 421 GAGTTGTCTGACAGCAGAAATCATGATCTTTTCTTCTCAACAACTTGCAGAAAGT 480
|||||
Db 610 ttaagaagtaaggaa 624
|||||
QY 481 TTAAGAAGTAAGGAA 495
|||||

RESULT 9

ID N30062 standard; DNA; 941 BP.
AC N30062;
DT 14-JUN-1992 (first entry)
DE Sequence of a modified BamHI human interferon-alpha gene fragment.
KW Yeast expression vector; Saccharomyces cerevisiae; promoter;
KW glycolytic enzyme; phosphoglycerate kinase; ss.
OS Homo sapiens.

FH Key Location/Qualifiers
FT CDS 7..534
FT /tag= a

PN EP--/73635-A.
PD 09-MAR-1983.
PF 17-AUG-1982; 408826.
PR 25-AUG-1981; GB-025934.
PR 23-MAR-1982; GB-008422.
PR 16-JUN-1982; GB-017496.
PA (KING/) KINGSMAN A J.
PA (CELL-) CELLTECH LTD.
PI Kingman S M; Kingman A J.
DR WPI; 83-25586K/11.
DR P-PSDB; P30163.
PT Yeast expression vector for transforming yeasts - useful in
PT economic proth. of polypeptide(s) esp. human interferon-alpha
PS Example; Fig 16; 45pp; English.
CC The inventors claim a yeast expression vector comprising a yeast
CC selective marker, a yeast replication origin and a yeast promoter
CC positioned relative to a unique restriction site. The yeast
CC promoter pref. comprises at least part of the 5' region of a gene
CC coding for glycolytic enzyme, esp. of the yeast PGK gene located up-
CC stream of the unique restriction site and at least part of the 3'
CC region of the PGK gene located downstream of the site. The vector
CC is used to express a polypeptide, eg. human interferon-alpha.
SQ Sequence 941 BP; 315 A; 184 C; 179 G; 263 T;

DB 3; Score 491; Match 99.5%; OryMatch 99.2%; Pred. No. 3.03e-308;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Db 37 tgtgatctgcttcaaacaccagcctgggtagcagagagaccttgatgctctctggcacag 96
|||||

Qy	1	TGTGATCGCCTCAAAACCCACAGCCTGGGTACGAGGAGCACCTGATGCTCTCTGGCACAG	60
Db	97	atgaggaataatctctcttttctcgttgctgaagcagacagcatgactttgattcccccag	156
Qy	61	ATGAGGAGATCTCTCTTTCTCTGCTTGAAGCAGACAGCTGACTTTGGATTTCCCCAG	120
Db	157	gaggagtttggcaaccagttccaaaaggctgaaccatccctgtctcccatgagatgac	216
Qy	121	GAGGAGTTTGGCAACGAGTTCCTAAAAGGCTGAACCATCCCTGTCTCCATGAGATGATC	180
Db	217	cagcagatcttcaatctcttcagcacaagaagcactcatctgctgttgggatgagacccctc	276
Qy	181	CAGCAGATCTTCAATCTCTTTCAGCACAAAGGACTCATCTGCTGTGGGATGAGACCTC	240
Db	277	ctagacaattctacactgaactctaccgcagctgaatgacctggaagcctgtgtgata	336
Qy	241	CTAGACAAATTTACACTGAACTCTACGACGAGCTGAATGACCTTGGAGCCTGTCTGATA	300
Db	337	cagggggtgggggtgacagagactcccctgatgaaggagactccattctggctgtgagg	396
Qy	301	CAGGGGGTGGGGGTGACAGACATCCCCCTGATGAAGAGGAGACTCCATTTGGCTGTGAGG	360
Db	397	aaatactccaagaadaactctctatctgaaagagaagaataacagcccttgtgctcgg	456
Qy	361	AAATACTTCCAAAGATCACTCTCTATCTTGAAAGAGAGAANAATACGCCCTTGTGCCTGG	420
Db	457	gaggttgtagcagcagaaatcatgagatcttttctgtcacaacttgcagaagt	516
Qy	421	GAGGTTGTGACGACAGAAATCATGAGATCTTTTCTTTGTGTCAACAACTTGCACAAAGT	480
Db	517	ttaagaaagtaaggaa	531
Qy	481	TTAAGAAGTAAGGAA	495

RESULT	10	
ID	N40013	standard; DNA; 503 BP.
AC	N40013;	
DT	30-NOV-1991	(first entry)
DE	DNA encoding recombinant interferon-alpha A.	
KW	Recombinant interferon-alpha A; ss DNA; antiviral.	
EH	Key	Location/Qualifiers
FT	CDS	6
FT	/tag= a	
FT	misc_feature	12..503
FT	/tag= b	
FT	/note= "claimed sequence"	
FT	EP-128467-A.	
PD	19-DEC-1984.	
PF	30-MAY-1984;	106214.
PR	01-JUN-1983;	US-499964.
PR	(HOFF) F Hoffmann-La Roche & Co.	
PI	DeChiara TM, Tarnowski SJ Jr.	
PI	WPI; 84-313909/51.	
DR	P-PSDB; P40022.	
DR	New antiviral interferon polypeptide(s) free from oligomers - with	
PT	cysteine residues replaced by other amino acid residues.	
PT	Disclosure; Fig. 1; 46pp; English.	
PS	The DNA encodes recombinant interferon-alpha A (rIFN aA). In this	
CC	protein, Cys 1 may be replaced by a glycine residue, and Cys 98,	
CC	99 or 100 may be replaced by Ser. These polypeptides have antiviral	
CC	activity, but unlike prior interferons they are free from	
CC	oligomers, other than dimers, and they pref. consist of stable	

[illegible]

RESULT	11	
ID	Q04744	standard; DNA; 573 BP.
AC	Q04744;	
DT	11-OCT-1990	(first entry)
DE	Sequence encoding hybrid Hu-IFN alpha A/gamma.	
KW	Hu-IFN; interferon; tumour; cancer; ds.	
OS	Homo sapiens.	
Key		Location/Qualifiers
FT	CDS	1..546
FT	/*tag= a	
PN	EP-372707-A.	
PD	13-JUN-1990.	
PF	27-OCT-1989;	311108.
PR	28-OCT-1988;	US-264271.
PA	(PEST/)	Pestka S.
PI	Pestka S;	
DR	WPI; 90-180507/24.	
DR	P-PSDB; R05400.	
PT	Phosphorylated modified proteins, including modified interferon(s) -	
PT	used in diagnostic and therapeutic applications. eg.	
PT	pharmacokinetic studies and tumour treatment.	

PS Claim 8; Fig 3; 47pp; English.

CC Hybrid IFN-gamma and IFN-alpha can be phosphorylated to a high

CC radio specific activity which IFN-alpha alone cannot.

CC By introducing phosphorylatable groups, the proteins may be used in

CC pharmacokinetic studies and diagnostic applications, by attaching 32P

CC labels to the incorporated sites.

DB 1; Score 491; Match 99.6%; QryMatch 99.2%; Pred. No. 3.03e-308;
Matches 493; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

DB 4 tgtgatctgcctcaaacccacacagctgggtagcagagagaccttgatgctctggccacag 63
|||||
QY 1 TGTATCTGGCCTCAACCCACAGCGCTGGGTACGAGAGGACCTTATGCTCTGGGCACAG 60
|||||
DB 64 atgagaaaaatctcttttctcctgcttgaagcagacatgacttttgatttccccag 123
|||||
QY 61 ATGAGAGAAATCTCTCTTTTCTCTGCTTGAAGGACAGCGTGACTTTGGATTTCCCCAG 120
|||||
DB 124 gaggadtgtgcaaccagcttccaaaaggctgaaacccatccctgtcctccatgagatgac 183
|||||
QY 121 GAGGAGCTTGGCAACCAAGTTCMAAAGCGTGAAGCAATCCCTGCTCCTCATGAGATGATC 180
|||||
DB 184 cagcagatcttcaatctcttcagcacaaaggactcatctgctgtgggatgagaccctc 243
|||||
QY 181 CAGCAGATCTCAATCTCTTCAGCACAAAGGACTCATCTGCTTGGGATGAGACCTC 240
|||||
DB 244 ctgacaaaattctacactgaactctaccagagctgaatgacctggaagcctgtgtgata 303
|||||
QY 241 CTAGACAAATTTACACTGACTCTACAGAGAGCTGAATGACCTGAGAGCCTGTGTGATA 300
|||||
DB 304 cagggggtgggggtgcagagagactccctctgatgaaggagactccattctgctgtgaag 363
|||||
QY 301 CAGGGGTGGGGGTGCAGAGAGACTCCCTCTCATGAAGGAGAGACTCCATTCTGGCTGTGAGG 360
|||||
DB 364 aaatacttccaaagaatcactctctatctgaaagagaagaatacagcccttgtgcctgg 423
|||||
QY 361 AAATACTTCCAAAGAATCACTCTATCTCAAAAGAGAGAAATACAGGCCCTTGTGCTGG 420
|||||
DB 424 gaggtgtcagagcagaatacatgagatcttttctttgtcaacaaactgtcagaagaagt 483
|||||
QY 421 GAGGTTGTCAGAGCAGAAATCATGAGATCTTTTCTTTGTCAACAAACTTCCAGAGAACT 480
|||||
DB 484 ttaagaagtaaggaa 498
|||||
QY 481 TTAAGAAGTAAAGAA 495
|||||

RESULT 12

ID Q11141 standard; DNA; 540 BP.

AC Q11141;

DT 03-JUN-1991 (first entry)

DE Interferon alpha as CR2 ligand.

KW Cellular receptor 2; CR2; binding site; BS; auto-immune disease;

KW Epstein-Barr Virus; EBV; B lymphocyte; ligand; interferon alpha; ss.

OS Synthetic.

FT Key Location/Qualifiers

FT CDS 58..507

FT /*tag= a

FT /product= interferon alpha

FT misc RNA 274..303

FT /*tag= b

FT /label= BS

FT /note= *fragment pref. included*

FT	misc RNA	283...315	
FT	/*tag= c		
FT	/label= BS		
FT	/note= "fragment most pref. included"		
PN	W09103251-A.		
PD	21-MAR-1991.		
PF	04-SEP-1990; U05027.		
PR	08-SEP-1989; US-404679.		
PR	20-APR-1990; US-512118.		
PA	(CALB-) CALIF INST BIOLOGIC.		
PI	Lernhardt W;		
DR	WPI; 91-101864/14.		
DR	P-PSDB; R11355.		
PT	DNA segment encoding CR-2 ligand and CR2 binding site - used to		
PT	treat auto-immune disease, B-cell lymphoma and inhibit		
PT	Epstein-Barr virus infection		
PS	Disclosure; Fig 2; 129pp; English.		
CC	The production of CR2 ligands including a binding site (BS) is		
CC	possible by transforming a cellular host with a recombinant DNA		
CC	mol. contg. this sequence. The ligand pref. includes a fragment		
CC	encoded by a sequence indicated in the features.		
CC	The ligand pref. contains only a single BS and has an		
CC	amino acid sequence <100 (pref. <20) residues in length.		
CC	The ligand may also comprise a plurality of the indicated segment		
CC	(tag c).		
CC	A therapeutic compen. contg. the polypeptide is used to stimulate		
CC	or inhibit B lymphocyte proliferation in patients with B cell		
CC	lymphoma. B lymphocytes and myeloma's can be stimulated in		
CC	patients with immunodeficiencies and immunoglobulin secretion by		
CC	hybridoma cultures can be boosted.		
CC	The compen. can be administered to inhibit infection in vitro or in		
CC	vivo by Epstein-Barr Virus.		
CC	See also Q11140-42.		
SQ	Sequence 540 BP; 153 A; 123 C; 132 G; 132 T;		
DB 2;	Score 487; Match 99.2%; QryMatch 98.4%; Pred. No. 1,61e-305;		
Matches 491; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
Db	13 tqtgatctgcctcaaaaccacagcctgggtacagaggagcattgactcctcctggcacag 72		
Qy	1 TGTGATCTGCCTCAAAACCCACAGCGCTGGGTAGCAGAGGACCTTGATGCTCTCTGGCACAG 60		
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Qy	121 CAGAGGTTTGGCAGACCACTTCNAAAGCTGAAACCATCCCTGCTCCATGAGATGATC 180		
Db	193 cagcagatcttcaactctcttcagcacaaaaggactcatctgctgttgggatgagaccctc 252		
Qy	181 CAGCAGATCTTCAATCTCTTCAGCAGAAAGGACTCATCTGCTGCTTGGGATGAGACCCCTC 240		
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Qy	241 CTACACAAAATTCTACACTGAACCTTACAGCAGCTGAAATGACCTGGAAGCCTGTGTGATA 300		
Db	313 caggggggtgggggtgacagagactcccttgatgaaggaggaactccattctggctgtgagg 372		
Qy	301 CAGGGGGTGGGGGTCACAGACATCCCTCTGATGAAGGAGGACTCCCATTTCTGGCTGTGAGG 360		
Db	373 aaataacttccaaaagaatcactctctatctgaaagagaagaatacacagccttctgtgctgg 432		

PT and neoplastic diseases
 PS Disclosure; Fig 1; 54pp; English.
 CC This hybrid DNA fragment is encoded by the replicable expression
 CC vector plasmid ple-IFA and may be expressed in *Escherichia coli* for
 CC production of the peptide. See also N20006-12, N20026-30 and P20008-
 CC 14.
 CC Sequence 958 BP; 266 A; 213 C; 191 G; 288 T;
 DB 4; Score 487; Match 99.2%; OryMatch 98.4%; Pred. No. 1.61e-305;
 Matches 491; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Db 130 tgtgatctgcctcaaaaccacagcctgggtacgaggagaccttgatgctcctggcacag 189
 Qy 1 TGTGATCTGCCTCAAAACCACAGCCTGGGTACGAGGAGGACCTTGATGCTCCCTGGCACAG 60
 Db 190 ataggaaatctctcttttctctgcttgaaaggacagacatgacttggattccccag 249
 Qy 61 ATGAGGAGAAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGACTTTGGATTCGCCAG 120
 Db 250 gaggagttggcaaccagttccaaaggctgaaacacccctctgctccatgagatgac 309
 Qy 121 GAGGAGTTGGCAACACAGTTCCAAAGGCTGAACCATCCCTGCTCCATCAGATGATC 180
 Db 310 cagcagatcttcaatctcttcagcacaaggagactcatctgcttgggatgagaccctc 369
 Qy 181 CAGCAGATCTTCAATCTCTCAGCACAAGGACTCATCTGCTGGTGGATGAGACCCCTC 240
 Db 370 ctgacaaattctacactgaactctaccagcagctgaatgacctggaagcctgtgtgata 429
 Qy 241 CTAGCAAAATTTACACTCAACTCTACCAGCAGCTGAATGCACTTGAAGCCTGCTGTGATA 300
 Db 430 cagggggtggggtgacagagactccctctgatgaaggaggactccattctgctgtgagg 489
 Qy 301 CAGGGGCTGGGGTGCACAGACTCCCTCTGATGAAGGAGGACTCCATTCTGGCTGAGG 360
 Db 490 aaatacttccaaagaatcaactctctatctgaaagaagaataacagcccttgcctgg 549
 Qy 361 AATATCTTCCAAAGATCACTCTCTATCTGAAGAGAAATACAGCCCTTGTGCTGG 420
 Db 550 gaggtgtcagagcagaatcatgagatcttttcttctgcaacaacttgcaagaagt 609
 Qy 421 GAGGTTGTACAGCAGAAATCATGATCTTTTCTTTGTCACAAACTTGCAAGAAAGT 480
 Db 610 ttaagaagtaacgaa 624
 Qy 481 TTAAGAAGTAAGGAA 495

RESULT 15

ID N20026 standard; DNA; 1109 BP.
 AC N20026;
 DT 18-DEC-1992 (first entry)
 DE Human leukocyte interferon.
 KW Leukocyte; interferon; antitumor; immunostimulant; virucide.
 OS Homo sapiens.
 PN EP--51873-A.
 PD 09-MAY-1982.
 PF 09-NOV-1981; 109579.
 PR 10-NOV-1980; US-205579.
 PR 23-FEB-1981; US-237388.
 PR 25-SEP-1981; US-305657.
 PA (GENE-) GENENTECH INC.
 PI Goeddel DVN;
 DR WPI; 82-41788E/21 (41788E).

PT Hybrid human leukocyte interferon(s) - useful for treating viral
 PT and neoplastic diseases
 PS Disclosure; Fig 9; 54pp; English.
 CC This DNA fragment may be expressed in *Escherichia coli* for
 CC production of human leukocyte interferon. IFN may be used
 CC for treating viral and neoplastic diseases. See also N20005-12,
 CC N20027-30 and P20007-14.
 CC Sequence 1109 BP; 307 A; 232 C; 223 G; 347 T;
 DB 4; Score 481; Match 99.4%; OryMatch 97.2%; Pred. No. 1.98e-301;
 Matches 494; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
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 Qy 1 TGTGATCTGCCTCAAAACCACAGCCTGGGTACGAGGAGGACCTTGATGCTCCCTGGCACAG 60
 Db 240 ataggagaatctctcttttctctgcttgaaggacagacatgacttggattccccag 299
 Qy 61 ATGAGGAGAAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGACTTTGGATTCGCCAG 120
 Db 300 gaggagtttaaggcaaccagttccaaaggctgaaacacccctgtcctccatgagatga 359
 Qy 121 GAGGAGTTT--GGCAACGAGTTCCAAAGGCTGAACCATCCCTGCTCCTCATGAGATGA 178
 Db 360 tccagcagatcttcaatctcttcagcacaaggagactcatctgcttgggatgagacc 419
 Qy 179 TCCAGCAGATCTTCAATCTCTTCAGCACAAGGACTCATCTGCTTGGGATGAGACCC 238
 Db 420 tccatagacaaattctacactgaactctaccagcagctgaatgaacctggaagcctgtgga 479
 Qy 239 TCCTAGACAAATTTCTACTGCACTCTACCAGCAGCTGAATGCACTTGAAGCCTGTGTGA 298
 Db 480 taccaggggtggggtgacagagactccctctgatgaaggaggactccattctgctgtga 539
 Qy 299 TACAGGGGCTGGGGCTCAGACAGACTCCCTCTGATGAAGGAGGACTCCATTCTTGGCTGTGA 358
 Db 540 ggaataacttccaaagaatcaactctctatctgaaagaagaataacagcccttgtcct 599
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 Qy 479 GTTTAAGAAGTAAGGAA 495

Search completed: Tue Aug 29 18:48:25 1995
 Job time : 40 secs.

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RESULT 3
LOCUS HSI6R6 742 bp RNA PRI 03-APR-1995
DEFINITION Human messenger RNA for leukocyte (alpha-2) interferon.
ACCESSION V00548
KEYWORDS complementary DNA; interferon; signal peptide.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Animalia; Metazoa; Chordata; Vertebrata; Mammalia;
Theria; Eutheria; Primates; Haplorhini; Catarrhini; Hominidae.
REFERENCE 1 (bases 1 to 742)
AUTHORS Streuli,M., Nagata,S. and Weissmann,C.
TITLE At least three human type alpha interferons: structure of alpha 2
JOURNAL Science 209 (4463), 1343-1347 (1980)
MEDLINE 81015442
COMMENT NCBI gi: 32740
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sig_peptide <1..51
/notes="reading frame (leader peptide)"
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mat_peptide 52..546
/notes="reading frame (interferon)"
polyA_site 742
/notes="polyA addition site"
BASE COUNT 202 a 170 c 168 g 202 t
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Db 103; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db 112 atgaggagaatctctcttttctctgcttgaaggacagacatgactttggatttccccag 171
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Qy 61 ATGAGGAGAAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGATTTGGATTTCCCG 120
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Db 172 gagagattggcaaccagttccaaaaggctgaaacacatccctgtctctcatgagatgac 231
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Db 232 cagcagatcttcaatctcttcagcaacaagagactcatctgctgttggtgagaccctc 291
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Qy 241 CTACAAAATTTCTACACTCAACTCTACAGCAGCTGAATGACCTGGAGCCTTGCTGATA 300
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Db 352 caggggttggtgggtgacagagactccctgatgaaggaggactccattctggcigtgagg 411
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Qy 301 CAGGGGCTGGGGCTGCACAGACACTCCCTCATGAAGAGGAGACTCCATTCTGCTCTCAG 360
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Db 412 aaatacttccaaagaatcactctctatctgaaagagaagaatacacagcccttgctgctgg 471
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Qy 361 AAATACTTCCAAAGAAATCACTCTCTATCTGAAGAGAGAAATACAGCCCTTGTCCTGG 420
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Db 472 gaggtgtgcagagcagaatcatgagatcttttcttctgtcaacaacttgcaagaagt 531
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Qy 421 GAGGTGTCAGAGCAGAAATCATGATCTTTTCTTCTCAACAACCTTGCAAGAAACT 480
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Db 532 ttaagaagttaaggaa 546
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Qy 481 TTAAGAAAGTAAGGAA 495
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RESULT 4
LOCUS I04187 1107 bp ss-DNA PAT 05-MAR-1993
DEFINITION Sequence 8 from patent US 4678751.
ACCESSION I04187
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1107)
AUTHORS Goeddel,D.V.
TITLE Hybrid human leukocyte interferons
JOURNAL Patent: US 4678751-A 8 07-JUL-1987;
Genentech, Inc.;
San Francisco, CA;

COMMENT NCBI gi: 268733
FEATURES
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BASE COUNT 305 a 232 c 223 g 347 t
ORIGIN

Db 93; Score 493; Match 99.8%; QryMatch 99.6%; Pred. No. 0.00e+00;
Matches 494; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Db 180 tgtgatctgtctcaaacccagacctgggtagcaggagaccttgatgctcctggcacag 239
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Db 240 atgaggagaatctctcttttctctgcttgaaggacagacatgactttggatttccccag 299
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Qy 61 ATGAGGAGAAATCTCTCTTTCTCTGCTTGAAGGACAGACGCTGATTTGGATTTCCCG 120
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Db 300 gagagattggcaaccagttccaaaaggctgaaacacatccctgtctctcatgagatgac 359
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Qy 121 GAGGAGTTTGGCAACCAAGTTCCAAAAGGCTGAACCAATCCCTCTCTCATGAGATGATC 180
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